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SEQUENCE FROM N.A.

SEQUENCE TISSUB=Brain;

STRAIN=C57BL/6; TISSUB=Brain;

STRAIN=C57BL/6; TISSUB=Brain;

STRAIN=C57BL/6; TISSUB=Brain;

STRAIN=C57BL/6; TISSUB=1247932;

STRAIN=C57BL/6; TISSUB=1247932;

RA STRAIN=C57BL/6; Dubmed=1247932;

RA STRAIN=C57BL/6; Dubmed=1247932;

RA STRAIN=C5.

A Colling F.S., Wagner L., Shenmen C.M., Schuler G.D., Antschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhard N.K., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C., Brab S.S., Worley N.A., Peters G.J., Abramson R.D., Mullahy S.J., Raha S.S., Worley K.J., McEwan P.J., McKernan K.J., Malek J.A., Gab L.J., Hulyk S.W., Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G., Abrames Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Grimwar J., Myers R.M., Butterfield Y.S., Raysyninski M.I., Syalska U., Smailus D.E., Schnerch A., Schein J.E.,
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                                                                                                     Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                   the EMBL/GenBank/DDBJ databases
                                                        CRC64;
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Mismatches:
Indels:
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Matches:
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                                              Hypothetical protein.
SEQUENCE 545 AA; 59679 MW;
                                                                                                                                                                                US-09-270-437D-7 (1-1946) x Q7TQF9
STRAIN=C57BL/6; TISSUE=Brain;
                                                                                         1.52e-87
1299.00
74.58%
61.05%
          Strausberg R.;
Submitted (JUL-2003) to the
EMBL; BC054552; AAH54552.1;
                                                                                                                                 Best Local Similarity:
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Pred. No.:
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RAP SEQUENCE FROM N.A.

A Zhang J.Y., Chan E.K., Peng X.X., Tan E.M.;

RADLINE=99207072; PubMed=10190901;

RAT "A novel cytoplasmic protein with RNA-binding motifs is an autoantigen

RT "In human hepatocellular carcinoma.";

C. -- SIMILARITY: CONTAINS 4 KH DOMAINS.

C. -- SIMILARITY: CONTAINS 4 KH DOMAINS.

C. -- SIMILARITY: CONTAINS 4 KH DOMAINS.

C. C: Cytoplasm; TAS.

GO: 00003735; R: RNA binding; TAS.

GO: 00007345; P: Pembryogenesis and morphogenesis; TAS.

GO: 00007345; P: Pembryogenesis and morphogenesis; TAS.

GO: 0000386; P: translational attenuation; TAS.

GO: 0000388; KH type-1.

DR Fam; PF00013; KH; 4.

Enerpro: IPR004089; KH; 4.

Enerpro: IPR004089; KH; 4.

Enerpro: IPR00322; KH; 4.

Enerpro: IPR00322; KH; 4.

Enerpro: IPR00322; KH; 4.

ENERPRO: SMART; SM00360; RRM; 2.

ENERPRO: SMART; SM00360; RRM; 2.

ENERPRO: ENERPRO: ENEW; 2.

ENERPRO: ENEWRY 2.

ENEWRY: SM00360; RRM; 2.

ENEWRY: SM00360; RRM; 2.

ENEWRY: SM00360; RRM; 2.

ENEWRY: SM00360; RRM; 2.

ENEWRY: ENEWRY: ENEWR; 2.

ENEWRY: 
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GluAlaHisIleLysValProSerPheAlaAlaGlyArgValIleGlyLysGlyGlyLys
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                                TCCAAAGTTCGTATGGTTATCATCACGGCCGCGGGGGCCCCAATTCAAGGCTCAGGGA
                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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Best Local Similarity:
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RC SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

RC STRAIN-BB; TISSUE-Body;

RX ALSUSER R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,

Raha B.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

R Richards S., Worley R.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nillalon D.K., Murny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rithing M., Madan A., Young A.C., Shevohnorko Y., Bouffard G.G.,

Mithing M. M., Touchman J.W., Green E.D., Dickson M.C.,

R Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

K. Arnes S. J. Marves M.,

R Rodriguez A.C., Grimwood J., Smallus D.E., Schnerch A., Schein J.E.,

R Arnes M. M., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,

R Arnes M. M. A.,

R Arnes M. M. Schalka U., Smallus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human and mouse CDNA securess."
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Vgl RNA binding protein (Decapentaplegic and Vg-related 1, RNA binding
                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes; Cyprinidae, Danio.
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SEQUENCE FROM N.A.
Zhang Q., Yaniv K., Oberman F., Wolke U., Git A., Fromer M.,
Taylor W., Meyer D., Standart N., Raz E., Yisraeli J.K.;
"YQI REP intracellular distribution and evolutionarily conserved expression suggest multiple roles during development.";
Mech. Dev. 0:0-0(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMARI, SMYGGOV, ALLY, KH TYPE_1; 4. PROSITE; PS550084; KH TYPE_1; 4. PROSITE; PS50102; RRM, 2. GROGIENCE 582 AA; 63351 MW; 9DAE63200681B306 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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GO; GO:0003676; F:nucleic acid binding; IEA.
InterPro; IPR004087; KH dom.
InterPro; IPR004088; KH type_1.
InterPro; IPR005094; RNA_rec_mot.
Pfam; PF00013; KH; 4.
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SMART; SM00322; KH; 4.
SMART; SM00360; RRM; 2.
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                                                                                  JVR1RBP
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582
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                         Conservative:
Mismatches:
      Length:
Matches:
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      6.96e-127
1830.50
82.19%
72.41%
51.84%
                                    Similarity:
                           Percent Similarity:
Alignment Scores:
                                              Query Match
                                     Best Local
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1092 CAGGIGITIALCCCCGCCCAGGCAGIGGCGCCALCATCAGGAGGAAGAAGGGGCAGCACATC 1151
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                        ThrSerAla&laCysLysSerIleLeuGluIleMetHisLysGluAlaGlnAsp1leLys
                                                                        ACGGCTGACGAGGTTCCCCTGAAGATCCTGGCCCATAATAACTTTGTAGGGCGTCTCATT
                                                                                         TCCTCGTTGCAAGACCTTACCCTTTACAACCCTGAGAGGACCATCACTGTGAAGGGGGCCC
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| AsnAspIleAlaSerMetAsnLeuGlnAlaAsnLeuIleProGlyLeuAsnLeuAsnAla
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SEQUENCE TROUB—AND, TISSUB—Thymus;

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A The FANTOM Consortium,

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A The RIEN Genome Exploration Research Group Phase I & II Team;

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Sciurognathi, Muridae, Murinae, Mus.
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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                    NCBI_TaxID=10090;
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Q8C2J9;
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Q1-MAR-2003 (TrEMBLrel. 23, Created)
Q1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
Q1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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P SEQUENCE FROM N.A.
STATAN=C57BL/6; TISSUE=Brain, and Olfactory epithelium;
Strausberg R.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
-: SIMILARITY: CONTAINS 4 KH DOWAINS.
REMBL; AKO11689; BAB19779.1; -.
REMBL; BC046173; BAB19755.1; -.
REMBL; BC046173; BAB19755.1; -.
REMBL; BC0461138; AAH45138.1; -.
REMBL; BC049082; AAH45138.1; -.
REMBL; BC049082; AH45082.1; -.
ROS; GO:0003676; F:nucleic acid binding; IBA.
InterPro; IPR0040087; KH-4ppe.1.
R InterPro; IPR004089; KH-4ppe.1.
R InterPro; IPR004089; KH-4ppe.1.
R Pfam; PF000076; RTM; 2.
SMART; SM00320; KH; 4.
SMART; SM00320; RH; 4.
SMART; SM00320; RH; 4.
SMART; SM00320; RH; 4.
R PROSITE; PS50084; KH-7PE.1; 4.
R PROSITE; PS50084; KH-7PE.1; 4.
SRQUENCE 579 AA; 63574 MW; CABD9A4355B392B7 CRC64;
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         411 PhelleProAlaLeuSerValGlyAlaIleIleGlyLysGlnGlyGlnHisIleLysGln
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                                                                              TCCTCCGCTTGTAAGATGATCTTGGAGATTATGCATAAAGAGGCTAAGGACACCAAAACG
                                                                                                                   GCTGACGAGGTTCCCCTGAAGATCCTGGCCCATAATAACTTTGTAGGGCGTCTCATTGGC
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SEQUENCE FROM N.A.

STRAINS-C57BL/6; TISSUB-Brain, and Olfactory epithelium;

STRAINS-C57BL/6; TISSUB-Brain, and Olfactory epithelium;

MEDLINE-2238825; PubMed=1247932;

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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 15, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
10 days embryo cDNA, RIKEN full-length enriched library,
clone:2610036B18, full insert sequence (Igf2 mRNA-binding protein (Insulin-like growth factor 2, binding protein 3).
(Insulin-like growth factor 2, binding protein 3).
Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus.
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PRT;
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                      Chordata, Craniata, Vertebrata, Euteleostomi, Primates, Catarrhini, Hominidae, Homo.
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Putative RNA binding protein KOC (KOC)
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                Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                        NCBI_TaxID=9606;
                                                                                                   TISSUE=Pancreas;
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                                                                                                    A Havin L., Git A., Elisha Z., Oberman F., Yaniv K.,
A Preseman Schwartz S., Standart N.M., Yisraeli J.K.;
Genes Dev. 0.0-0(1998).
--- SIMILARITY: CONTAINS 4 KH DOMAINS.
REMEL, AF042353, AA4897457.1; --
REMEL, AF042353, AA4897457.1; --
REMEL, AF046433, AA408957.1; --
GO, GO: 0003676; F:nucleic acid binding; IEA.
RINEERPO; IPRO04089; KH dom.
RINTERPO; IPRO0504; RNA_rec_mot.
RITHERPO; IPRO076; KH; 4.
REMEL; SM00325; KH; 4.
SMART; SM00360; RRM, 2.
SMART; SM00360; RRM, 2.
REMEL; PS50084; KH TYPE 1; 4.
REMSITE; PS50084; KH TYPE 1; 4.
REMSITE; PS50030; RRM, 1; FALSE NEG.
REMSITE; PS50030; RRM; 1; FALSE NEG.
REMSITE; PS50030; RRM; 1; FALSE NEG.
                   SEQUENCE FROM N.A.
Griffin D., Taylor W.L.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
10-OCT-2003 (TrEMBLrel. 25, Last annotation update)
KH domain-containing transcription factor B3.
Xenopus laevis (African clawed frog).
Xenopus hetazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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Pfaff S.L., Taylor W.L.;
"Characterization of a Xenopus oocyte factor that binds to a
developmentally regulated cis-element in the TFIIIA gene.";
Dev. Biol. 151:306-316(1992).
                ATGAAGAAAGTTCGGGAGGCCTATGAGAATGATGTGGCTGCCATGAGC--
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
VGI RNA binding protein variant D.
Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Amphibia, Batrachia; Anura, Mesobatrachia; Pipoidea, Pipidae;
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MEDLINE=98228351; PubMed=9560341;

MEDLINE=98228351; PubMed=9560341;

Deshler J.O., Highet M.I., Abramson T., Schnapp B.J.;

T A highly conserved RNA-binding protein for cytoplasmic mRNA localization in vertebrates.";

Curr. Biol. 8489-49611998).

C +i - SIMILARITY: CONTAINS 4 KH DOMAINS.

R EMBL, ARF054923; AAC41285.1; -..

R GO; GO:0003676; F:nucleic acid binding; IEA.

R InterPro; IPR004089; KH type I.

InterPro; IPR004089; KH type I.

InterPro; IPR004089; RNA_rec_mot.
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Havin L., Git A., Elisha Z., Oberman F., Yaniv K., Pressman Schwartz S., Standart N.M., Yisraeli J.K. Genes Dev. 0:0-0(1998).
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NCBL_TaxID=8355;
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                                                                                                                                                            Conservative:
Mismatches:
                                                                                                                               Length:
Matches:
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Pfam; PF00013; KH; 4.

Pfam; PF00076; rrm; 2.

SMART; SM00322; KH; 4.

SMART; SM00360; RRM; 2.

PROSITE; PS50084; KH TYPE_1; 4.

PROSITE; PS50102; RRM; 2.
                                                                                    65643 MW;
                                                                                                                               1.29e-137
1975.50
85.60%
75.24%
55.95%
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PROSITE; PS50102; RRM; 2.
PROSITE; PS00030; RRM_RNP_1; FALSE_NEG.
SEQUENCE 576 AA; 63271 MW; 01AAF2D1D81C8811
                                                                                                                                                                                                                                           US-09-270-437D-7 (1-1946) x 042254 (1-576)
                                                                                                      2.87e-168
2389.50
96.59%
94.39%
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Best Local Similarity:
Query Match:
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Pred. No.:
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WE SEQUENCE FROM N.A.

WEDLINE=97220007; PubMed=9121465;

A ROSS A.F., Oleynlkov Y.S., Kislauskis E.H., Taneja K.L., Singer R.H.;

A ROSS A.F., Oleynlkov Y.S., Kislauskis E.H., Taneja K.L., Singer R.H.;

"Characterization of a beta-actin mRNA zipcode-binding protein.";

"Colono Contains 4 KH DOMAINS.

"REMBL; ARD6557; RAB82295.1; - .

"REMBL; ARD6356; F:nucleic acid binding; IEA.

"InterPro; IPR004088; KH-type-1.

"Rems, PF00013; KH; 4.

"DR Pfam; PF00013; KH; 4.

"DR SMART; SM00320; KH; 4.

"DR SMART; SM00320; KH; 2.
  SerLeuGlnSerHisLeuIleProGlyLeuAsnLeuAlaAlaValGlyLeuPheProAla 378
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                                        TCATCCAGCGCAGTCCCGGCCTCCCAGCGTTACTGGGGCTGCTCCCTATAGCTCC
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Gallus gallus (Chicken).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
NCBI_TaxID=9031;
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Last sequence update)
Last annotation update)
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Matches:
Conservative:
Mismatches:
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2,9e-175
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98.80%
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Query Match:
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SEQUENCE FROM N.A.

STRAIN=129/Sv x 129/Sv-CP; TISSUE=Embryonic stem cells;

STRAIN=129/Sv x 129/Sv-CP; TISSUE=Embryonic stem cells;

RA MISSUES BREAT, Perhapold E.A., Grouse L.H., Derge J.G.,

RA Aleschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Aleschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Aleschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Back S.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Back S.A., McEwan P.J., McKernan K.J., Abzamson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Villalon D.K., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

RA Richards S., Malan J.W., Stenen E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Stenen E.D., Dickson M.C.,

RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,

Jones S.J., Maria M.A.,

RA "Generation and initial analysis of more than 15,000 full-length human modes Control of the control of t
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Sciurognathi, Muridae, Murinae; Mus
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SPRAIN-129/Sv. 129/Sv-CP; TISSUE-Embryonic stem cells; Strausberg R.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC051679; ARH51679.1; -.
GO:0003676; F:nucleic acid binding; IEA.
InterPro; IPR004089; KH dom.
InterPro; IPR004089; KH type_1.
InterPro; IPR004089; KH type_1.
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Last sequence update)
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Mammalia; Eutheria; Rodentia;
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01-JUN-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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Pfam; PF00076; rrm; 2.
SMART; SM00322; KH; 4.
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SMART; SMO0360; RRM; 2.
PROSITE; PS501004; KH TYPE_1; 4.
PROSITE; PS501002; RBM; 2.
SEQUENCE 577 AA, 63378 MW; D439F544257DA3CE CRC64;
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Matches:
Conservative:
Mismatches:
Indels:
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347 158 407 178 467 198 527 218 587 238 647 258 707 278 767 298 827 318 887

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AGCCTGCTGGCTCAGTATGGTACAGTAGAGAACTGTGAGCAAGTGAACACCGAGAGTGAG
                    ThralavalValAsnValThrTyrSerAsnArgGluGlnThrArgGlnAlaIleMetLys
                                                                                         CTGAATGGCCACCAGTTGGAGAACCATGCCCTGAAGGTCTCCTACATCCCCGGATGAGCAG
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2 STRAIN=C273EL/6J;

2 Mally SEQUENCE FROM N.A.

3 The FANTOM Consortium,
3 The FANTOM Consortium,
4 The FANTOM Consortium,
5 The RIKEN Genome Exploration Research Group Phase I & II Team;
5 Thallysis of the mouse transcriptome based on functional annotation of an arture 420:563-573 (2002).

3 EMBL; ARC44860; BAG32119.1;

3 DR MGI:1890357; Igf2bpl.

3 DR MGI:1890357; Igf2bpl.

4 DR MGI:1890357; Igf2bpl.

5 DR MGI:1890357; Igf2bpl.

6 OG:0003676; F:nucleic acid binding; IEA.

6 DR MGI:1890357; Iff Adom.

7 DR MGI:1890357; Iff Adom.

8 DR MGI:1890357; Iff Adom.

8 DR MGI:189032; KH; 4.

8 SMART; SM00322; KH; 4.

8 SMART; SM00322; KH; 4.

8 SMART; SM00360; RRM; 2.

8 SROUENCE 577 AA; 63378 MW; D75897450841532E CRC64;
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AlaGIyArgVall1eGlyLysGlyGlyLysThrValAsnGluLeuGlnAsnLeuThrAla
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                                       TTCTTTGGTCCCAAGGAGGAAGTGAAGCTGGAGACCCACATACGTGTGCCAGCATCAGCA
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1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Insulin-like growth factor 2.
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                 Conservative:
Mismatches:
Indels:
            Length:
Matches:
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Alignment Scores:
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                                                                                           CTGAATGGCCACCAGTTGGAGAACCATGCCCTGAAGGTCTCCTACATCCCGGATGAGCAG
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 168 AGCCTGCTGGCTCAGTATGGTACAGTAGAGAACTGTGAGCAAGTGAACACCGAGAGTGAG
                                                                                                                                        ATAGCACAGGGGCCTCGAGAATGGGCCCCCGGGGGCCTTTGGCTCTCGGGGTCAGCCCCCGC
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MEDLINE=92217743; PubMed=1559612;
Bernstein P.L., Herrick D.J., Prokipcak R.D., Ross J.;
"Control of c-myc mRNA half-life in vitro by a protein binding to a coding region stability determinant.";
Genes Dev. 6:642-654(1992).
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01-NOV-1998 (TYEMBLrel. 08, Created)
01-NOV-1998 (TYEMBLrel. 08, Last sequence update)
01-NOV-1998 (TYEMBLrel. 25, Last annotation update)
01-NOT-2003 (TYEMBLrel. 25, Last annotation update)
Coding region determinant binding protein.
IGF2BPI OR CRDBP.
Mus musculus (Mouse)
Ebukaryota, Metacoa, Chordata, Craniata, Vertebrata, E
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae,
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MEDITINE=9415886; PubMed=8114742;
Herrick D.J., Ross J.;
"The half-life of c-myc mRNA in growing and influence of the coding and 3' untranslated ribosome translocation.";

ribosome translocation.";
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SMART; SM00322; KH; 4.
SMART; SM0360; RRM; 2.
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OBNZIB;
OBNZIB;
O1-OCT-2000 (TREMBLrel. 15, Last sequence update)
O1-OCT-2003 (TREMBLrel. 15, Last annotation update)
MRNA-binding protein CRDBP.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
WCBI_TAXID=9606;
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"Ectopic expression of a KH-domain containing protein, highly homologous to both human IMP-1 and mouse CRD-BP, in benign and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     malignant mesenchymal tumors.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases
-!- SIMILARITY: CONTAINS 4 KH DOMAINS.
EMBL, AF198254; AAF37203.1; --
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GO; GO:0003676; F:nucleic acid binding; JILTEPPO; IPR004087; KH dom.
InterPro; IPR004088; KH type_1.
InterPro; IPR00504; KNĀ_rec_mot.
Pfam; PF00013; KH; 4.
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Pfam; PF00076; rrm; 2.
SMART; SM00322; KH; 4.
SMART; SM00360; RRM; 2.
PROSITE; PS50104; KH TYPE_1; 4.
PROSITE; PS50102; REM; 2.
SEQUENCE 577 AA; 63436 MW; 0647676128FBDIEE CRC64;
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Matches:
Conservative:
Mismatches:
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Q9cpn8 mus musculu Q9cpn8 mus musculu Q9c2j9 mus musculu Q9v6m1 homo sapien Q7tqf9 mus musculu Q9v6m2 drosophila Q8ir99 drosophila Q8ir99 drosophila Q8igk4 drosophila Q21605 caenorhabdi Q9c553 arabidopsis Q7tp50 rattus norv
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Q23487 caenorhabdi
Q7z145 caenorhabdi
Q7zvk5 brachydanio
Q8ax85 xenopus lae
P91391 caenorhabdi
Q85791 oryza sativ
Q85791 oryza sativ
Q9bla0 caenorhabdi
Q7xx1 xenopus lae
Q9x13 arabidopsis
Q96x6 homo sapien
O82762 arabidopsis
Q17936 caenorhabdi
Q17936 caenorhabdi
                                    Q8brh1 mus musculu
Q80us9 mus musculu
Q42254 gallus gall
O73932 xenopus lae
O57526 xenopus lae
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Ogfnk3 arabidopsis
Ogli28 oryza sativ
Ogldv1 arabidopsis
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Q95sz9 drosophila
Q9w702 xenopus lae
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    sapien
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Bom T., Singer R.H., Bassell G.J.;
Enor T., Singer R.H., Bassell G.J.;
Molecular interactions between rZBP1 and b-actin zipcode required for transport of mRNA and stimulation of spine growth.";
Submitted (Aug-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AF541940; AAO16210.1;
GO: GO:0003676; Finucleic acid binding; IEA.
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116,
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Last annotation update)
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
B-actin zipcode binding protein 1.
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Q8IR99
Q8IGK4
Q21605
Q9C553
Q7TP50
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Q7ZVK5
Q8AX85
P91393
Q8S7G1
Q8LNT9
Q9BLA0
Q7ZXS1
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Q9LXF5
Q96EP6
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Q17935
Q17936
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Q80US9
O42254
O73932
O57526
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Q9PWB0
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Q7TQF9
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Q8LDV1
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Q23487
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InterPro; IPR004088; KH_type_1.
InterPro; IPR000504; RNA_rec_mot.
Pfam; PF00013; KH; 4;
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  QBCGX0
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-MODEL=frame+ n2p.model -DEV=xlp
-O=/cgn2 1/USFTO spool p/USO9270437/runat 23072004 095739 27425/app query.fasta_1.5582
-D=SPTREMBL_25 - OEWT=fastan -SUFFIX=rspt -MINMATCH=0.1 -LGOPEXT=0
-UNITG=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITG=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=USG09270437 @cGN 1 1 287 @runat _23072004 095739 _27425 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSFBLOCK=100 -LONGLOG
-DEV_TIMBOUT=120 -WARN_TIMBOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8cgx0 rattus norv
                                                                                                                                     July 23, 2004, 10:55:00; Search time 93.0388 Seconds (without alignments) 13198.757 Million cell updates/sec
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3531
1 gctgtagcggagggggctggg......atttccttcaggttttaaaa 1946
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                   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                  OM nucleic - protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of hits satisfying chosen parameters:
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Listing first 45 summaries
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sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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sp_fungi:*
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sp_invertebrate:*
sp_mammal:*
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Maximum DB seq
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38	886	430	470	965	490	1019	510	1066	530	126	50	1186	570		
418 nGlulleArgLysArgThrAsnAlaAsnIleCysIleSerLysGlyLysLysAspAspLe 438	IACCCTTTACAACCCTGAGAGGACCATCACTGTGAAGGGGGCCATCGAGAATTGTTGCAG	urreneral de la composition della composition de	::: ::: :::::	GAGCTCTCACCTGATCCCT	:::::: AlaThrArgLysProProAlaArgThrAspAsnCysSerPheLeuSerGlySerSerAs	GGCCTGAACCTGGCTGTAGGTCTTTTCCCAGCTTCATCCAGGGCAGTCCCG 1		CGCCTCCCAGCGTTACTGGGGCTGCTCCCTATAGCTCTTAT	510 yTyrGlySerPheProAlaGlyAspAsnValLeuGlySerThrGlyProTyrSerTyrGl 5	GCAGGCTCCCGAGCAGGAGGTGCAGGTGTTTATCCCCGCCCAGGCAGTGGCGCCAT 1126	:::	CATCGGCAAGAAGGGCACACATCAAACAGCTCTCCCGGTTTGCCAGGCCTCCATCAA		1187 GATTGCACCCGGAAACA 1205	: ::: ulleSerLysThr 576
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Search completed: July 23, 2004, 11:06:27 Job time: 41.1191 secs

InterPro; IPR004088; KH_type_1

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STRAINE-CV. Columbia;

MEDLINB=22954850; PubMed=14593172;

A Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,

A Southwick A.M., Wu H.C., Xim C.J., Nguyen M., Pham P.K., Cheuk R.F.,

A Rarlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,

A Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,

A Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,

A rakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,

Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,

Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,

Khan S., Koesema B., Ishida J., Jiang P.X., Jones T., Kawai J.,

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Yuan S., Shinozaki K., Davis R.W., Theologis A., Boker J.R.;

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dabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A.,
Neumann S., Argiriou A., Vitale D., Liguori R., Piravandi E.,
A Massenet C., Quigley F., Clabauld G., Muendlein A., Felber R.,
Schnabl S., Hiller R., Schmidt W., Lecharry A., Aubourg S.,
Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
A Gibbons T., Weber N., Vandenbol M., Bargues M., Tarcol J., Torres A.,
RA Heijnen L., Schwarz S., Scholler P., Heber S., Francs P., Bielke C.,
RA Fishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
RA Arnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
Schokon M., Murray J., Sheet P., Cordes M., Abu-Threadeh J.,
Stocking T., Kalicki J., Graves T., Harmon G., Edwards J.,
A Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Kramer J., Fulton L., Mardis E., Dante M., Peppin K., Hillier L.W.,
RA Markoniu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
A Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
Swaby I.K., O'Shaugnessy A., Rodriguez M., Hoffman J., Till S.,
RA Chen E., Marka M.A., Martiensen R., Hammed A., Lodhi M., Johnson A.,
RA "Siguence and analysis of chromosome 4 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORMS 1 AND 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 402:769-777(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thaliana.
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Insoid=P58223-2; Sequence=VSP 008899, VSP 008900;
Note=May be due to a competing acceptor site. No experimental confirmation available;
-!- SIMILMENTY: Contains 5 KH domains.
-!- CAUTION: Ref.1 sequences differ from that shown due to erroneous gene model prediction. At4g18370 and At4g18375 were originally fused into a single gene.
                                                                                                                                                                                                       IsoId=P58223-1; Sequence=Displayed;
Note=No experimental confirmation available;
                                                                                                                                 Event=Alternative splicing; Named isoforms=2;
genome.";
Science 302:842-846(2003).
Science 302:842-846(2003).
-!- SUBCELLULAR LOCATION: Nuclear (Potential).
                                                                                                                                                                              Name=1
                                                                                                                                                                                                                                                                                 Name=2
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EMBL; ALO21710; CAA16717.1; ALT_SEQ.
EMBL; AL161248; CAB78839.1; ALT_SEQ.
EMBL; AX133701; AAM91635.1; --
EMBL; BT001108; AAN64172.1; --
                                                                                              EMBL; BT001108; AAN64172.1;
InterPro; IPR004087; KH_dom.
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598
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358 uCysValllelleValThrAlaThrGluSerProAspAspMetLysSerMetAlaValGl
                                                                                                                                                                                                                                                                                                                       125 AATCCGAAATATTCCACCCCAGCTCCGATGGGAAGTACTGGACAGCCTGCTGGTCAGTA
                                                                                                                                                                                                                                                                                                                                                                                        ::: |||::: ||| |||||| || ||||| || GlnAspHisIleLeuGlnGlyAlaGlyValProSerTyrPheAsnAla------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----LeuSerValSerAspPheGlnGly
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                                                                                                                                                                                                                                                                                                                                             218 AsnbroArgGluAsnIleProLeuAspSerThrSerGlnAspValProAlaAlaSerVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       359 ACCIGAGAAIGGGGGCGCGAGGGGCTTIGGCICICGGGGTCAGCCCCGCCAGGGCTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                        239 GAATGTCACCTATTCCAACCGGGAGCAGCAGGCAAGCCATCATGAAGCTGAATGGCCA
      PROBLEM PRODOLS; KH; 5. SWART; SW00312; KH; 5. SWART; SW00312; KH; 5. PROSTUR; PS50084; KH TYPE 1; 5. Hypothetical protein; Nuclear protein; RNA-binding; Repeat; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                          185 TGGTACAGTAGAGAACTGTGAGCAAGTGAACACCGAGAGTGAGACGGC
                                                                                                                                                                            61F135BB8647C0C CRC64;
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89
80
164
10
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KH 2.

KH 3.

KH 4.

KH 5.

L -> F (in isoform 2).

/FTIG=VSP_008899.
                                                                                                                                                  Missing (in isoform 2) /FIId=VSP 008900.
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Conservative:
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Best Local Similarity:
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532
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1052

SO THE PRESENTATION OF THE PROPERTY OF THE PRO

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1053 TATAGCTCCTTTATGCAGGCTCCCGAGCAGGAGATGGTGCAGGTGTTTATCCCCGCCCAG 1112
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MEDLINE=20083488; PubMed=10617198;

MEDLINE=20083488; PubMed=10617198;

MEDLINE=20083488; PubMed=10617198;

MAPER K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,

Rad Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N.,

Harris B., Ansorgew, Brandt P., Girvell L., Rieger M.,

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Nos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P.,

Langham S.-A., McCullagh B., Bilham L., Robben J.,

Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,

Neitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,

Holzer E., Brandt A., Peters S., van Staveren M., Hauf J., Koetter P.,

Mociman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,

Berneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,

Van Monitagu M., Rogers J., Cronin A., Quail M.A., Bray-Ahlen S.,

Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,

Pettett A., Rajandeam M.A., Lyne M., Benenst T.-H.,

Borkova D., Blocker H., Schaefer M., Meller-Auer S.,

Dose S., de Haan M., Maarse A., Schaefer M., Mueller-Auer S.,
    272 GlyAlaHislleLyslleGly---AsnGlnAlaGluGlyAlaGlyGluArgHisValThr 290
                                                                                                     885 AGGGCCGAGCAGGAAATGAAGAAAGTTCGGGAGGCCTATGAGAATGATGTGGCTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              252 LeulleGlyCysVallleGlyArgGlnGlySerLysIleSerGlulleArgGlnMetSer
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                                                                                                                                                                                                                                                                                                                                                                                      218 GlnLeuSerSerHisAlaValProPheAlaThrProSerValValProGlyLeuAspPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238 GlyThr------GinThrSerSerGinGluPheLeu------ValProAsnAsp
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Putative mucleic acid binding protein At4918375.
AT4G18375 OR F2B012.2.
Arabidopsis thaliana (Mouse-ear cress).
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                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the ENTODEAN Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTGGACATCCCCCTTCGGCTCCTGGTGCCCACCCAGTATGTGGGTGCCATTATTGGCAAG 512
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nucleic acid binding protein that binds
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ThrThrIleThrGlySerThrAlaAlaValPheHisAlaValSerMetIleAlaPheLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     765 AACCTGAAGAAGGTAGAGCAAGATACCGAGACAAAATCACCATCTCCTCGTTGCAAGAC
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PROSITE; PS50084; KH TYPE 1; 3.
Nuclear protein; RNA-binding; Ribonucleoprotein; DNA-binding;
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36 LysGlyGluThrValLysArglleArgGluGlnSerAlaArgIle-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3D99F762A9471265 CRC64;
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80
53
114
65
                    preferentially to oligo dC (By similarity).
SUBCELLULAR LOCATION: Muclear (By similarity).
SIMILARITY: Contains 3 KH domains.
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Mismatches:
Indels:
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Matches:
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EMBL; AK03993; BAB14761.1; -.
EMBL; BC003008; AAH03008.1; -.
EMBL; BC004153; AAH03108.1; -.
Genew; HGNC:8652; PCBP4.
Go; GO:0000543; C:nucleus; ISS.
GO; GO:000377; F:DNA binding; ISS.
GO; GO:001671; P:DNA binding; ISS.
INTERPRO; IPRO04087; KH dom.
INTERPRO; IPRO04088; KH_CYPE.1.
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  FUNCTION: Single-stranded
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217.50
42.63%
25.64%
6.16%
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Best Local Similarity:
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101
241
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Pred. No.:
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Db 723LysGlnThrLysSerPheThrValAspl Qy	Oy 1551 CAGCAGCATCAGAAGGGACAGAGTAACCAGG ::: ::: Db 798 pasnValValGluAspSerMetLeuValAsp RESULT 14 PCB4 HUMAN ID PCB4 HUMAN STANDARD; PRT; 40:				RA Ninomiya K., Iwayanagi T.; RT "NEDO human cDNA sequencing project."; RL Submitted (AUG-2000) to the EMBL/GenBan RN [3] RP SEQUENCE FROM N.A. RC TISSUE=Lung; RX MEDILINE=22388257; PubMed=12477932; RA Strausberg R.L., Feingold E.A., Grouse	RA Klausner R.D., Collins F.S., Wagner L. RA Altschul S.F., Zeeberg B., Buetow K.H. RA Hopkins R.F., Jordan H., Moore T., Max RA Diatchenko L., Marusina K., Farmer A.A RA Stapleton M., Soares M.B., Bonaldo M.F RA Brownstein M.J., Usdin T.B., Toshlyuki RA Raha S.S., Loquellano N.A., Peters G.J RA Bosak S.A., McEwan P.J., McKernan K.J.	RA Richards S., Worley K.C., Hale S., Garc RA Villalon D.K., Wurny D.M., Sodergren E. RA Fahey J., Helton E., Ketteman M., Madan R., Ketteman M., Radwing M.C., Shevc RA Blakesley R.W., Touchman J.W., Green E. RA Rodriguez A.C., Grimwood J., Schmutz J. RA Butterfield Y.S.N., Krzywinski M.I., Sk Schnerch A., Schein J.E., Jones S.J.M., RT "Generation and initial analysis of mor RT human and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-
::::		594 GAAAAAGCCATCAGTGTACCACCCCTGAGGGCTGCTCCTCCGCTTGTAAGATGATC 653 553IleValGlnLeuargGlyProLysAsnGluValGluLysCysThrLysTyr 569 654 TTGGAGATTATGCATAAAGAGGCTAAGGACACCAAAACGGCTGACGAGGTTCCCTGAAG 713 550 MetGlnLysMetValalaAspLeuValGluAsnSerTlyrSerIleSerValProIlePhe 589	714 ATCCTGGCCCATAATAACTTTGTAGGGGGTCTCATTGGCAAGGAAGG	834 TACAACCCTGAGAGGACCATCACTGTGAAGGGGCCATCGAGAATTGTTGCAGGGCC 890	GCCTGAACCTG ::: AsnIle CCAGCAGCGTT	GCTCCCGAGCAGGAGTGTTTATCCCCGCCCAGGAGTGGGCGCCATCATC	
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CGAGTTGCAGAATTTGACGGCAGCTGAGGTG 1430
                                                                                                                  GAACGACCAGGTCATCGTGAAATCATCGGA 1490
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                                                                                                                                              plleArgAlaLysProGluTyrHisLysPhe 741
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L., Shenmen C.M., Schuler G.D.,
H., Schaefer C.F., Bhat N.K.,
Max S.I., Wang J., Hsieh F.,
A.A., Rubin G.M., Hong L.,
M.F., Casavant T.L., Scheetz T.E.,
M.F., Abramson R.D., Mullahy S.J.,
G.J., Abramson R.D., Mullahy S.J.,
G.J., Malek J.A., Gunarature P.H.,
Garcia A.M., Gay L.J., Hulyk S.W.,
m E.J., Lu X., Gibbs R.A.,
nadan A., Rodrigues S., Sanchez A.,
hevchenko Y., Bouffard G.G.,
T. Wyers R.M.,
Skalska U., Smailus D.E.,
Skalska U., Smailus D.E.,
more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amma T., Otsuki T., Suzuki Y., Shiratori A., Sudo H., Sodaira H., Kondo H., Sugawara M., Aurakawa K., Ono Y., Takiguchi S., Ishii S., Kawai Y., Saito K., Y., Nagahari K., Masuho Y.,
                                                                n genes establishes a subfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1, Vertebrata; Euteleostomi;
ini; Hominidae; Homo.
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|spProLysHis 811
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A REDLINE=22388257; PubMed=12477932;

A Lausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Capleton M., Soares M.B., Bonaldo M.F., Caraninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Dosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Human and mouse cDNA sequences: ",

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
LeuAsnGlnValAlaArgGlnGlnSerHisPheAlaMetMetHisGlyGlyThrGlyPhe 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SECUENCE FROM N.A.
MEDLINE=92291094; PubWed=1318310;
MCKnight G.L., Reasoner J., Gilbert T., Sundquist K.O., Hokland B.,
MCKernan P.A., Champagne J., Johnson C.J., Bailey M.C., Holly R.,
O'Hara P.J., Oram J.F.,
"Cloning and expression of a cellular high density lipoprotein-binding
protein that is up-regulated by cholesterol loading of cells.";
J. Biol. Chem. 267:12131-12141(1992).
                                                                                                         ::: ::: ::: |||
258 AlaGlyIleAspSerSerProGluValLysGlyTyTTpAlaSerLeuAspAlaSer
                                                                                     1077 GAGCAGGAGATGGTGCAGGTGTTTATCCCCGCCCAGGCAGTGGGCGCCCATCATCGGCAAG
                              TATAGCTCCTTTATGCAGGCTCCC
                                                                                                                                                                                                                                                           1257 TTCAAGGCTCAGGGAAGAATCTATGGCAAACTCAAGGAGAAACTTCTTTGGT 1310
                                                                                                                                                                                                                                                                                      337 SerLeuAlaGlnTyrLeuileAsnAlaArgLeuSerSerGluLysGlyMetGly 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Vigilin (High density lipoprotein-binding protein) (HDL-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION.
MEDLINE=96184515; PubMed=8605996;
Kugler S., Grunweller A., Probst C., Klinger M., Muller P.K.,
                                                                                                                                                                                                                                                                                                                                                  PRT; 1268 AA
                            1029 AGCAGCGTTACTGGGGCTGCTCCC----
                                                                                                                                                                                                                                                                                                                                                              000341; Q9UCY3;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequ
10-OCT-2003 (Rel. 42, Last ann
                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                423 GlnIleGluGlyMetValLysAspLeuIleAsnArgMetAspTyrValGluIleAsnIle 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --AAGGTCTCCTACATCCCC 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    255 AACCGGGAGCAG-------ACCAGGCAAGCCATCATGAAGCTGAAT---
                         nuclear localisation sequence and is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50084; KH TYPE 1; 14.
HDL; Lipid transport; Cholesterol metabolism; RNA-binding; Repeat;
                                                                                      -!- FUNCTION: APPEARS TO PLAY A ROLE IN CELL STEROL METABOLISM. IT MAY FUNCTION TO PROTECT CELLS FROM OVER-ACCUMULATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL) (POTENTIAL)
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109
81
191
113
                                                                                                                                                           SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches:
Conservative:
Mismatches:
Kruse C.;
"Viglin contains a functional nuclear localisat
present in both the cytoplasm and the nucleus.";
FEBS Lett. 382:330-334(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phosphorylation; Nuclear protein; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIM; 142695; ...
GO; GO: 0005886; C: plasma membrane; TAS.
GO; GO: 0008289; F: lipid binding; TAS.
GO; GO: 0008203; F: cholesterol metabolism; TAS.
InterPro; IPR004087; KH_dom.
InterPro; IPR004088; KH_Lype_1.
FRAM: PF00013; KH; 14.
SMART; SM00322; KH; 12.
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KH 13.
KH 13.
KH 13.
KH 13.
KH 14.
                                                                                                                                                                                  SIMILARITY: Contains 14 KH domains.
SIMILARITY: STRONG, TO C.ELEGANS C08H9.2.
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22.06%
6.17%
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588
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PDB; 1VIH; 03-APR-96.
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EMBL; AJ003023; CAA05814.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       1254 CAATTCAAGGCTCAGGGAAGAATCTATGGCAAACTC------AAGGAGAGAACTTC 1304
                                                                                                                                                                                                                                                                                                                                                   1194 CCACCCGAAACACCTGACTCCAAAGTTCGTATGGTTATCATCACTGGACCGCCAGAGGCC 1253
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      ----GCTTCATCCAGCGCA 1013
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                                                                                                                            LeuAlaAlaAlaAlaSerAlaAsnProAlaAlaAlaAlaAlaAsnLeuLeuAlaThr
                                                                                                                                                                                                                                                               1134 AAGAAGGGGCAGCACATCAAACAGCTCTCCCGGTTTGCCAGCGCCTCCATCAAGATTGCA
                                                                                                                                                                            1074 CCCGAGCAGGAGATGGTGCAGGTGTTTATCCCCGCCCAGGCAGTGGGCGCCATCATCGGC
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Lagomorpha, Leporidae, Oryctolagus.
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Poly(xC)-binding protein 1 (Alpha-CP1) (hnRNP-E1)
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|LeuProAsnSerThrGluArgAlaIleThrIleAlaGlyValProGlnSerValThrGlu 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           426 GCGGGGGCCCCAGCCAAGCAGCAGCAAGTGGACATCCCCCTTCGGCTCCTGGTGCCCACC 485
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|LeuArgLeuValValProAlaThrGlnCysGlySerLeuIleGlyLysGlyGlyCysLys
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120 IleLysGluIleArgGluSerThrGlyAlaGlnValGlnValAlaGly-----AspMet
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| SerGlyAlaArgIleAsnIle-----SerGluGlyAsnCysProGluArgIleIle
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                                            InterPro; lPKNULL...
Pfam; PF00013; KH; 3.
SMART; SM00322; KH; 3.
PR0STTE; PS50084; KH; TYPE 1; 3.
PR0STTE; PS50084; KH TYPE 1; 3.
Nuclear protein; NNA-binding; Ribonucleoprotein; DNA-binding; Repeat.
DOMAIN 13 75 KH 1.
TH 1.
TH 2.
TH 2.
TH 3.
TH 3.
TH 3.
TH 3.
TH 4.
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75
75
139
69
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Matches:
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HSSP; Q07244; IKHM.
InterPro; IPR004087; KH_dom.
InterPro; IPR004088; KH_type_1.
                                                                                                                                                                                                                                                                                                                         2.62e-06
218.50
41.90%
20.95%
6.19%
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                                                                                                                                                                                                                                                                                                   Isold-P51513-3; Sequence=VSP_002842;
TISSUE SPECIFICITY: Brain.
DISEASE: Autoantigen in the paraneoplastic opsoclonus myoclonus attaxia (POMA), a paraneoplastic neurological syndrome/disorder (PNS/D) associated with breast cancer, fallopian cancer, and SCLCa and characterized primarily by loss of inhibitory control of motor neurons in the spinal cord and brainstem. Recognized by the IgG autoantibody ANNA-2 (also called anti-Ri).
                                                                                                                                Structure 7:191-203(1999).

-!- FUNCTION: May regulate RNA splicing or metabolism in a specific subset of developing neurons.

-!- SUBCELLUIAR LOCATION: Nuclear.

-!- ALTERNATIVE PRODUCTS:

EVent-Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00322; KH; 3.
PROSITE; PS50084; KH_TYPE_1; 3.
Antigen; Nuclear protein; RNA-binding; Repeat; Alternative splicing;
                                                                                                                                                                                                                                                         Name=2; Synonyms=Tumor;
IsoId=P51513-2; Sequence=VSP_002841, VSP_002843, VSP_002844;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BIPARTITE NUCLEAR LOCALIZATION SIGNAL
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                                       X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 423-495.
MEDLINE=99148126; PubMed=10368286;
Lewis H.A., Chen H., Edo C., Buckanovich R.J., Yang Y.Y.-L.,
Musunuru K., Zhong R., Darnell R.B., Burley S.K.;
"Crystal structures of Nova-1 and Nova-2 K-homology RNA-binding
Kavsan V.M.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; 138489; 138489.
PIR; 10-MAY-00.
Genew; HGNC: 7886; NOVAI.
GK; PS1513; ---
MIM; 602157; ---
GO; GO:0003723; F:RNA binding; TAS.
GO; GO:000526; F:NOCOMOTORY behavior; TAS.
GO; GO:0002880; F:RNA splicing; TAS.
GO; GO:000268; P:SYNAptic transmission; TAS.
                                                                                                                                                                                                                                             IsoId=P51513-1; Sequence=Displayed;
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KH 3.
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InterPro; IPR004088; KH type 1
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SMART; SM00322; KH; 3.
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88
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VARSPLIC
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Alignment Scores:

Query Match: DB: .. 00 à 셤 d d à В qq g ద à à à ò ò ö ďΩ à d ð 셤 ð a à g à a g ð à g à Missing (in isoform 2).
/FTIG=VSP 002841.
Missing (in isoform 3).
/FTIG=VSP 002842.
VKIIVPNS -> KHNISMIS (in is /FTIG=VSP 002843.
/FTIG=VSP 002843.
/FTIG=VSP 002844.
/FTIG=VSP 002844. 52055 MW; 510 AA;

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458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 AsnValAlaLysThrGluProValSerIleLeuGlnProGlnThrThrValAsnProAsp 148
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AlaAlaGlyLeuLeuGlyHisAlaAsnLeuAlaGlyValAlaAlaAlaPheProAlaValLeu 307
                                                                                                                                                                                                                                                                                                    ProLeuGluAlaProProGluAlaGlySerThrLysArgThrAsnThrGlyGluAspGly 48
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                                                                                                                                                                                                                                                                                                                                              ---ATCCCCCTTCGGCTCCTGGTGCCCACCCAGTATGTGGGTGCCATTATTGGCAAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                               CCCCGCCAGGGCTCACCTGTGGCAGCGGGCCCCCAGCCAAGCAGCAGCAAGTGGAC---
                                                                                                                                                                                                                                                                                                                                                                  49 GlnTyrPheLeuLysValLeuIleProSerTyrAlaAlaGlySerlleIleGlyLysGly
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Length:
Matches:
Conservative:
                                                              Mismatches:
                                                                                Indels:
                                                                                                                                        US-09-270-437D-7 (1-1946) x NOA1 HUMAN (1-510)
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      1.86e-06
                    221.50
34.89%
21.64%
6.27%
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                                       Percent Similarity:
Best Local Similarity:
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GCTGAGGTGGTAGTACCAAGA-----GACCAGACCCCTGGATGAGAACGACCAGGTCATC 1475
                                                                                                               GCAGTCCCGCCGCCTCCCAGCAGCGTTACTGGGGCTGCTCCCTATAGCTCCTTTATGCAG 1070
                                                                                                                                                                    1071 GCTCCCGAGCAGGAGATGGTGCAGGTGTTTATCCCCGCCCAGGCAGTGGGCGCCATCATC 1130
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                                                                                                                                                                                                                                                  --GlyThrPheAlaLeuGlySerLeuAlaAla 376
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TISSUE-Cerebellum, and Hippocampus;

MEDLINE=940000830; PubMed=8398153;

Buckanovich R.J., Posner J.B., Darnell R.B.;

"Nova, the paraneoplastic Ri antigen, is homologous to an RNA-binding protein and is specifically expressed in the developing motor
                                                                               419 ValGlyAlaIleLeuGlyLysGlyGlyLysThrLeuValGluTyrGlnGluLeuThrGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            290 LeuSerGlyPheThrGlyAsnAspLeuValAlaIleThrSerAlaLeuAsnThrLeuAla
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                                                                                                                                                                                                                                                                                                                               1251 GCCCAATTCAAGGCTCAGGGAAGAATCTATGGCAAACTC-----AAGGAGGAGAAAC
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                                                                                                                                                                                                                                                                                                                                                                                    302 ITCTTTGGTCCCAAGGAGGAAGTGAAGCTGGAGACCCACATACGTGCCCAGCATCAGCA
                                                                                                                                                                                                                                                                                                                                                                                                           403 ThrAspGlySerLysAspValValGlu------IleAlaValProGluAsnLeu
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                                                              GCTTCATCCAGC
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01-0CT-1996 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
RNA-binding protein Nova-1 (Neuro-oncological ventral antigen 1)
neuron-specific protein 1).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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IISSUE=Fetal brain;
Dmitrenko V.V., Garifulin O.M., Shostak K.A., Smikodub A.I.,
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01-0CT-1996
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|ProMetThrThrSerArgAlaAsnGlnValLySIleIleValProAsnSerThrAlaGly 170
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230 AspProGlnSerGlySerCysLeuAsnIleSerTyrAlaAsnValThrGlyProValAla
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|SerArgLysArgProLeuGluAlaProProGluAlaGlySerThrLysArgThrAsnThr
                                                                                                                                                                                                                                                                                                             ACCCCTGAGGGCTGCTCCTCCGCT------TGTAAGATGATCTTGGAGATTATG
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191 ValGinLeuSerGinLysProAsp---GlyIleAsnLeuGinGluArgValValThrVal
                                                                                                                                                                                                                                                                                                                                                                                                                      ---AAGATCCTGGCCCATAATAACTTTGTAGGG
                                                                                                                                                                                                                                                                                              CAAGTGGAC----ATCCCCCTTCGGCTCCTGGTGCCCACCCCAGTATGTGGGTGCCATT
BIPARTITE NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                     493
107
69
167
151
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                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                            7D09E8A55B0A7817
                                                                                                                                                                                                               US-09-270-437D-7 (1-1946) x NOA1_MOUSE (1-493)
                         KH 1.
KH 2.
ALA-RICH.
KH 3.
                                                                              MW,
                    102
223
395
474
50302 M
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                                                                                                                                221.50
35.63%
21.66%
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                         35
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 13
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138 LeuProAsnSerThrGluArgAlaIleThrIleAlaGlyValProGlnSerValThrGlu 157
                                                              888 GCCGAGCAGGAAATA-----ATGAAGAAAGTTCGGGAGGCCTATGAATGAT 935
                                                                                       ::::::||| CysValLysGinIleCysLeuValMetLeuGluThrLeuSerGinSerProGinGlyArg 177
                                                                                                                                                                              178 ValMetThrIleProTyrGlnProMetProAlaSerSerProValIleCysAlaGlyGly 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/60; TISSUB-Cerbellum;
MEDLINE=22354683; PubMed=12466851;
Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               277 SerThrGlnThrThrHisGluLeuThrIleProAsnAsnLeuIleGlyCysIleIleGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=CBA/J; TISSUE=Brain;
MEDLINE=20458856; PubMed=11003693;
Mard-Bailey P.F., Wood B., Johnson K.R., Bronson R.T., Donahue L.R.,
Davisson M.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                new spontaneous mutation in the mouse.";
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                                                                                                                                          GIGGCIGCCATGAGCICICACCIGAICCCIGGCCIGAACCIGGCI--
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Mamm. Genome 11:820-823(2000)
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RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,

Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

Ballake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

Raballa E., Dragani T.A., Fatcher C.F., Forrest A., Forrer K.S.,

RA Garsterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

RA Magshima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

RA Ravasi T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

RA Ravasi T., Reed J.C., Reed D.J., Ring B.Z., Ringwald M.,

Sandelin A., Schneider C., Semple C.A., Serou M., Shimada K.,

Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

Naining L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,

Kan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,

RA Shiraki T., Maki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,

RA Hirozane Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,

RA Hirozane Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,

RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,

RA Hara A., Hashizume W., Imotani K., Ishii Y., Romo H.,

Birney E., Hayashizaki Y.,

Birney E., Hayashizaki Y.,

Birney E., Hayashizaki Y.,

Barnaysis of the mouse transcriptome based on functional annotation of Nature A., Nature M., Nature M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dredge B.K., Darnell R.B.;

T "Nova regulates GABA(N) receptor gamma2 alternative splicing via a distal downstream UCAU-rich intronic splicing enhancer.";

Mol. Cell. Biol. 23:4687-4700(12003).

-!- FUNCTION: Functions to regulate alternative splicing in neurons by binding pre-mRNA in a sequence-specific manner to activate exon inclusion. It binds specifically to the sequence UCAUY. Most likely acts to activate the inclusion of exon E3A in the glycine receptor alpha-2 chain and of exon E9 in gamma-aminobutyric-acid receptor gamma-2 subunit via a distal downstream UCAU-rich intronic splicing enhancer.

-!- Subschilula LOCATION: Nuclear.

-!- DISEASE: Defects in NOVAl leads to neuronal death in spinal and brainstem neurons.
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Okano H.J., Yang Y.Y.-L., Darnell R.B.;
"Nova-1 regulates neuron-specific alternative splicing and
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Nuclear protein; RNA-binding; Repeat.
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IDA.
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Neuron 25:359-371(2000).
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EMBL; AKC47565; BAC33088.1; -.
MGD; MGI:104297; Noval.
GO; GO:0005634; C:nucleus; IC.
GO; GO:0003729; F:mRNA binding; IDA
GO; GO:006371; P:mRNA binding; IDA
GO; GO:006371; P:mRNA binding; III
InterPro; IPR004089; KH dom.
InterPro; IPR004088; KH_type_1.
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SMART; SM0322; KH;
PROSITE; PS50084; K
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828 ACCCTTTACAACCCTGAGAGGACCATCACTGTGAAGGGGGCCATCGAGAATTGTTGCAGG 887
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Z29505; CAA82631.1; ALT_FRAME.
Q07244; 1KHM.
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EMBL; U24223; AAA91317.1;
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                                                                                    -----AAGGAGGAGAACTTCTTTGGTCCCAAGGAGGAAGTG 1325
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TISSUE SPECIFICITY: Abundantly expressed in skeletal muscle, thymus and peripheral blood leucocytes while a lower expression is observed in prostate, spleen, testis, ovary, small intestine, heart, liver, adrenal and thyroid glands.

PTM: PHOSPHORYLATED. THE NON-PHOSPHORYLATED FORM(S) EXHIBITED THE SIRONGEST POLY(RC) - BINDING ACTIVITY.

SIMILARITY: Contains 3 KH domains.

SAUTION: There is probably a frameshift error in the nucleotide sequence of Ref.3.
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MEDLINE=94203810; PubMed=8152927;
MEDLINE=94203810; PubMed=8152927;
MEDLINE=94203810; PubMed=8152927;
MEDLINE=94203810; Debmod=815.295.;
MEDLINESHORD TO TABLE TRANSCRIPT OF THE TRANSCRIPT OF
                                                                                                                     Kiledjian M., Wang X., Liebhaber S.A.;
"Identification of two KH domain proteins in the alpha-globin mRNP
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Leffers H., Dejgaard K., Celis J.E.; "Characterisation of two major cellular poly(rC)-binding human proteins, each containing three K-homologous (KH) domains."; Eur. J. Biochem. 230:447-453(1995).
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Nuclear protein; RNA-binding; Ribonucleoprotein; DNA-binding;
Phosphorylation; Repeat.
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KH 2.

KH 3.

V -> A (IN REF. 2 AND 3).

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GO; GO:0005737; C:cytoplasm; NAS.
GO; GO:0005634; C:nucleus; NAS.
GO; GO:0003723; F:RNA binding; IDA.
GO; GO:0003697; F:Single-etranded DNA binding; IDA.
GO; GO:0016071; P:mRNA metabolism; NAS.
InterPro; IPR004089; KH_type_1.
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                   Kumar D.V., Nighorn A., 51 John P.A.;

"Role of Nova-1 in regulating alpha2N, a novel glycine receptor

"Role of Nova-1 in regulating alpha2N, a novel glycine receptor

"Role of Nova-1 in regulating spinal cord neurons.";

J. Neurobiol. 52.156-165(2002).

-! FUNCTION: Functions to regulate alternative splicing in neurons by binding pre-mRNA in a sequence-specific manner to activate exon inclusion. It binds specifically to the sequence UCAUY (By similarity). Acts to regulate a novel glycine receptor alpha-2 chain splice variant (alpha-2N) in developing spinal cord.

-! SUBCELLULAR LOCATION: Nuclear.

-! SIBCLARITY: Contains 3 KH domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AY262017; AARZUCO.Z...,
INTERPRO; IPR004087; KH dom.
INTERPRO; IPR004088; KH-Type-1.
Pfam; PF00013; KH; 3.
SMART; SM00322; KH; 3.
PROSITE; PS50084; KH TYPE 1; 3.
ANTigen; Nuclear profein; RNA-binding; Repeat.
DOMAIN 26 42 RIPARTITE NUCLEAR LOCALIZATION SIGNAL
                                                                                                                                                          [1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN=BDIX; TISSUE-Cerebellum; STRAIN=BDIX; TISSUE-Cerebellum; Knudsen A., Monstad S.E., Vedeler C.A.; Knudsen A., the paraneoplastic Ri antigen, is associated with breast "Nova-1, the paraneoplastic Ri antigen, is associated with breast "norar.";
                                            10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
RNA-binding protein Nova-1 (Neuro-oncological ventral antigen 1)
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111B GGGCGCCATCATCGGCAAGAGCGCACCATCAAACAGCTCTCCCGGTTTGCCAGCGC 1177 245 aGlyLeuvallleGlyLySGlyGlyGlyGluThrIleLySGlnLeuGlnGluArgAlaGlyVa 265 1178 CTCCATCAAGATTGCCACCCCGAAACTCCCCAAAGTTCGTATGGTTATCAT 1234 265 lLyBMet1leLeulleGlnAspGlySerGlnAsnThrAsnValAspLySProleuArg11 285 1235 CACTGGACCGCAGAGCCCAATTCAAGGCTCAGGGAAGATCTATGGCTAAGGT 1234	1457 TGAGAACGAGGTCATCGTGAAAATCATCGGACATTTCTATGCCAGTCAGATGGCTCA 1516	
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Alignment Scores:
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437 yAlaArgIleGlnIleSerLysLysGlyGluPheLeuProGlyThrArgAsnArg---Ar 456
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                                         280 SerThrAlaLeuAsnThrLeuAlaSerTyrGlyTyrAsnThrAsnSerLeuGlyLeuGly
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                                                                                      1073 TCCCGAGCAGGAGATGGTGCAGGTGTTTATCCCCGCCCCAGGCAGTGGGCGCCCATCATCGG
                                                                                                                                                                            CAAGAAGGGCAGCACATCAAACAGCTCTCCCGGTTTGCCAGCGCCTCCATCAAGATTGC
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646-651, AND FUNCTION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97282621; PubMed=9136930;
Min H., Turck C.W., Nikolic J.M., Black D.L.;
A new regulatory protein, KSRP, mediates exon inclusion through
intronic splicing enhancer.";
Genes Dev. 11:1023-1036(1997).
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mouse chromosome 17.";
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FUBP2 OR KHSRP.
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                                                                                                                                                                                                                                                                             "Cooperative assembly of an hnRNP complex induced by a tissue-specific homolog of polypyrimidine tract binding protein."; Mol. Cell. Biol. 20:7479(2000).

-!-FUNCTION: Binds to the dendritic targeting element and may play a role in mRNA trafficking (By similarity). Part of a ternary complex that binds to the downstream control sequence (DCS) of the pre-mRNA. Mediates exon inclusion in transcripts that are subject to tissue-specific alternative splicing. May interact with single-stranded DNA from the far-upstream element (FUSE). May activate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Nuclear. A small proportion is also found in the cytoplasm of neuronal cell bodies and dendrites (By
                                           Davis-Smyth T., Duncan R.C., Zheng T., Michelotti G., Levens D.; "The far upstream element-binding proteins comprise an ancient family of single-strand DNA-binding transactivators."; J. Biol. Chem. 271:31679-31687(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Part of a ternary complex containing FUBP2, PTBP1, PTBP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity).

TISSUB SPECIFICITY: Detected in neural and non-neural cell lines.

MILLARITY: Contains 4 KH domains.

CAUTION: Ref.3 sequence differs from that shown due to numerous frameshifts.
                                                                                                                                                                            FUNCTION, AND INTERACTION WITH PTBP1; PTBP2 AND HNRPH1.
MEDLINE=20459250; PubMed=11003644;
Markovtsov V., Nikolic J.M., Goldman J.A., Turck C.W., Chou M.-Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWART; SM00322; An; T.

SMOSITE; PS50084; KH_TVPE_1; 4.

Transport; mRNA transport; mRNA processing; mRNA splicing;

Transport; mRNA transport; mRNA processing; mRNA splicing;

Transcription regulation; Trans-acting factor; Nuclear protein;

DNA-binding; RRA-binding; Repeat.

DOWAIN 233 299 KH 1.

DOWAIN 322 386 KH 3.

DOWAIN 322 489 KH 3.
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V -> G (IN REF. 2).
G -> G (IN REF. 2).
G -> A (IN REF. 2).
V -> G (IN REF. 2).
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TISSUE=B-cell lymphoma, and Skeletal muscle;
MEDLINE=97094955; PubMed=8940189;
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GLY-RICH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR004087; KH dom.
InterPro; IPR004088; KH_type_1.
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496
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                                                                                                                                                                                                                                                               Black D.L.;
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72709 MW;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UCAY-3'.
DISEASE: Autoantigen in the paraneoplastic opsoclonus myoclonus attaxia (PCMA), a paraneoplastic neurological syndrome/disorder (PNS/D) associated with breast cancer, fallopian cancer, and SCLCa and characterized primarily by loss of inhibitory control of motor neurons in the spinal cord and brainstem. Recognized by the IgG autoantibody ANNA-2 (also called anti-Ri).

SIMILARITY: Contains 3 KH domains.
                                                                            SEQUENCE OF 29-492 FROM N.A.

SEQUENCE OF 29-492 FROM N.A.

SEQUENCE OF 29-492 FROM N.A.

Burkhart-Schultz K.J., Gordon L., Dias J., Ramirez M., Stilwagen S.,

Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J.,

Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,

Attix C., Andreise T., Trankheim M., Amico-Keller G., Coefield J.,

Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,

Arellano A., Brower A., Sanders C., Ow D., Nolan M., Trong S.,

Kobayashi A., Olsen A.S., Carrano A.V.;

"Sequence analysis of a 1.9 Mb region in 19913.2 between APOE and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in a specific
Is single strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 405-491 IN COMPLEX WITH RNA.
MEDLINE=20139984; PubMed=10676814;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lewis H.A., Musunuru K., Jensen K.B., Edo C., Chen H., Darnell R.B., Burley S.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIM; 601991; -.
InterPro; IPR004088; KH_type_1.
InterPro; IPR04088; KH_type_1.
Ffam; PF00013; KH; 3.
SMMAT; SMO0322; KH; 3.
SMMAT; PR50084; KH TYPE 1; 3.
Antigen; Nuclear profein; RNA-binding; Repeat; 3D-structure.
DOMAIN 10 26 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Nuclear (By similarity).
TISSUE SPECIFICITY: Brain. Expression restricted to astrocytes.
DOMAIN: The third KH domain (KH3) recognizes specifically 5'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Sequence-specific RNA binding by a Nova KH domain: implications paraneoplastic disease and the fragile X syndrome."; Cell 100:232-332(2000).
-!- FUNCTION: May requiate RNA splicing or metabolism in a specif subset of developing neurons (By similarity). Binds single st
                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 405-480.
MEDLINE=99148126; PubMed=10368286;
Lewis H.A., Chen H., Edo C., Buckanovich R.J., Yang Y.Y.-L.,
Musunuru K., Zhong K., Darnell R.B., Burley S.K.;
"Crystal structures of Nova-1 and Nova-2 K-homology RNA-binding
                       a
S
                                                                                                                                                                                                                                                                                                                                 Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases
               "The neuronal RNA-binding protein Nova-2 is implicated autoantigen targeted in POMA patients with dementia."; Proc. Natl. Acad. Sci. U.S.A. 95:13254-13259(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U70477; AAB88661.1; ALT_INIT.
EMBL; AF083898; AAC72355.1; -
EMBL; AC065540; AAD13116.1; -.
PDB; 1DTJ; 18-FEB-00.
PDB; 1EC6; 07-APR-00.
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Darnell R.B.;
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MIM; 601991; -.
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Yin G.L.,
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260 GlyValGlyAlaPheProAlaAlaLeuProAlaPheSerGlyThrAspLeuLeuAlaIle 279
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| ProAspArgAlaLysGlnAlaLysLeuIleValProAsnSerThrAlaGlyLeuIleIle
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PAA -> TAT (IN REF. 1).
41B63EAF6899256B CRC64;
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118
62
185
1111
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Indels:
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Matches:
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ALA-RICH.
GLY-RICH.
KH 3.
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236.50
37.89%
24.84%
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492 AA;
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                                           1119
                                                                                                                                                                                                                                                                                                                                                             1384 GTGGAAAAACGGTGAACGAGTTGCAGAATTTGACGGCAGCTGAGGTGGTAGTACTACCAAGAG 1443
                                                                                                                                                                                                                                                                                                                                                                                                          ----AAAA 1482
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                                                                                      1120 GCGCCATCATCGGCAAGAAGGGCAACACCATCAAACAGCTCTCCCGGTTTGCCAGCGCCT 1179
                                                                                                                                                                             CACCCGAAACACCTGACTCCAAAGTTCGTATGGTT---------ATCATCA 1236
                                                                                                                                                                                                                                                                      CTCAGGGAAGAATCTATGGCAAACTCAAGGAGGAGAACTTCTTTGGTCCCAAGGAGGAAG 1323
                                                                                                                                                                                                                                                                                                                   TGAAGCTGGAGACCCACATACGTGTGCCAGCATCAGCAGCTGGCCGGGTCATTGGCAAAG 1383
CITCATCCAGCGCAGICCCGCCGCCTCCCAGCAGCGITACIGGGGCTGCTCCCTAIAGCT 1059
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                                                               -- IleAspvalProValProArgHisServalG 336
                                                                                                   roproAspArgCysGluHisAlaAlaArgIleIleAsnAspLeuLeuGlnSerLeuArgS 396
                                                                                                                                                                                                                                                                                                                                                                                                                        464 InLeuProProAsnGlyAspProAsnPheLysLeuPheValIleArgGlySerProGlnG 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       537 lyProProProHisGlnTyrProProGlnGlyTrpGlyAsnThrTyrProGluTrpGln 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------ProGlyGlyProGlyProAlaGlyProMetG
                                                                                                                                                    356 rgileGlnPheLysGlnAspAspGlyThrGlyProGluLysIleAlaHisIleMetGlyP
                                                                                                                                                                                                                                                                                                                                 erdlyProPro--GlyProProGlyAlaProGlyMetProProGlyGlyArgGlyArgGl
                                           1060 CCTTTATGCAGGCTCCCGAGCAGGAGATGGTGCAGGTGTTTATCCCCGCCCAGGCAGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           484 lnileAspHis-----AlaLysGlnLeuIleGluGluLysileGlu-----
                     ----serArgvalGly6lyGly--
                                                                                                                                                                                                                                                                                                                                                                                                          1444 ACCAGACCCCT----GATGAGAACGACCAGGTCATCGTG----
                                                                                                                                                                                                                                                                                        yArgGlyGlnGlyAsnTrpGlyProProGlyGlyGluMetThrPhe-
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                                                                                                                                                                                                                           CTGGACCGCCAGAGGCCCAATT-----
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||| SluSerLysLysLeuAlaAlaGlnGlyAspCysGluTyrGlyProArgGlyGlyAlaPro 154
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., SEQUENCE OF 104-119; 242-267; 679-685; 705-711 AND 743-766, FUNCTION, DEVELOPMENTAL STACE, AND SUBCELLULAR LOCATION.
MEDLINE=21640447; PubMed=11781334;
Gu W., Pan F., Zhang H., Bassell G.J., Singer R.H.;
Gu W., Pan F., Zhang H., Bassell G.J., Singer R.H.;
Gu W., Pan F., Zhang H., Bassell G.J., Singer R.H.;
Cal Biol. 156:41-52(2002).
-: FUNCTION: Binds to a 54-nucleotide localization signal (the zipcode) found in the 3' untranslated region of beta-actin mRNA and may play a role in its localization.
-: SUBCELLULAR LOCATION: Predominantly nuclear. Also detected in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           212 GAACACCGAGAGGGACGGCAGTGGTGAATGTCACCTATTCCAACCGGGAGCAGACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              272 GCAAGCCATCATGAAGCTGAATGGCCACCAGTTGGAGAACCATGCCCTGAAGGTCTCCTA
                                                                                                                                                                                                 Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytoplasm.

DEVELOPMENTAL STAGE: The highest expression is found in 6-d embryos, is reduced to 30% before hatching and remains stable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfan; PF00013; KH; KH; 4.
SMART; SM00322; KH; 4.
PROSITE; PS50084; KH TYPE 1; 4.
Transport; mRNA transport; Nuclear protein; RNA-binding; Repeat.
DOMAIN 208 272 KH 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    155 AlaAlaProProGluArgSerGlyProValGlyAspProProGlyPro-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF461020; AAL66365.1; -.
GO; GO:0005737; C:cytoplasm; IDA.
GO; GO:0005634; C:nucleus; IDA.
GO; GO:0003798; P:RRNA 3' UTR binding; IDA.
GO; GO:0008298; P:RNA localization, intracellular; NAS.
InterPro; IPR004087; KH_dom.
InterPro; IPR004088; KH_type_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         875A6C83529969EB CRC64;
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Matches:
Conservative:
Mismatches:
                                                      28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Zipcode-binding protein 2.
AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thereafter. SIMILARITY: Contains 4 KH domains.
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21.16%
6.73%
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   CHICK
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SEQUENCE
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                                                                                                                                                                                                                                                                                             Rehbein M., Wege K., Buck F., Schweizer M., Richter D., Kindler S.;
"Molecular characterization of MARTAI, a protein interacting with the dendritic targeting element of MARTAI, a protein interacting with the J. Neurochem. 82:1039-1046(2002).

-!- FUNCTION: Part of a ternary complex that binds to the downstream control sequence (DCS) of the pre-mRNA. Mediates exon inclusion in transcripts that are subject to tissue-specific alternative splicing. May interact with single-stranded DNA from the farupstream element (FUSE). May activate gene expression (By similarity). Binds to the dendritic targeting element and may play a role in mRNA trafficking.

-!- SUBUNIT: Part of a ternary complex containing FUBP2, PTBP1, PTBP2
                                                                                                                                                                                                      [1] -
SEQUENCE FROM N.A., SEQUENCE OF 73-87; 89-108 AND 475-486, SUBCELLULAR
LOCATION, AND FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and HNRPH1 (By similarity).
SUBCELLULAR LOCATION: Nuclear. A small proportion is also found in the cytoplasm of neuronal cell bodies and dendrites.
                                                                                                                                                     Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
                                                          XX.
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Far upstream element binding protein 2 (FUSE binding protein 2)
type splicing regulatory protein) (KSRP) (MAP2 RNA trans-acting protein 1) (MAP2 RNA trans-acting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFam; PF00013; ALI, 4.
SMART; SM00222; KH; 4.
PROSITE; PS50064; KH_TYPE 1; 4.
Transport; mRNA transport; mRNA processing; mRNA splicing;
Transcription regulation; Trans-acting factor; Nuclear protein;
DNA-binding; RNA-binding; Repeat.
DOMAIN 145 209 KH 1.
DOMAIN 323 387 KH 2.
NOMAIN 323 387 KH 2.
NOMAIN 323 387 KH 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRC64;
                                                                                                                                                   Sukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALA/GLY/PRO-RICH.
482C7A765C60EE4A
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GLY-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: Contains 4 KH domains.
                                                                                                                                                                                                                                                                                 MEDLINE=22246918; PubMed=12358751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF308818; AAG59811.1; -.
InterPro; IPR004087; KH_dom.
InterPro; IPR004088; KH_type_1.
                                                                                                                                                                   Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MM.
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                                                                                                                                  Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    721 AA;
                                                                                                                                                                                        NCBI_TaxID=10116;
                                                                                                              FUBP2 OR KHSRP
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721 151 75 221 276 29

Length:
Matches:
Conservative:
Mismatches:
Indels:

7.36e-08 244.50 31.26% 20.89% 6.92%

Best Local Similarity:

Query Match:

Percent Similarity:

US-09-270-437D-7 (1-1946) x FUB2_RAT (1-721)

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438
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                                                                GCCGGAAAATTCAAATCCGAAATATTCCACCCCAGCTCCGATGGGAAGTACTGGACAGCC 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 roProArgThrSerMetThrGluGluTyrArg-----valProAspGlyMetValGlyL 159
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|InAsnThrAsnValAspLysProLeuArgIleIleGlyAspProTyrLysValGlnGlnA 296
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                                                                                                  --ProGlyProProGlyAlaGlyAspArgGl 41
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GGCCTCAGCCCACCCAGAGGCCGGGGTGGGAGGCCGAGTCCTCAGCTTCCCCGGGTTAGGA
                                                                                                                                172 TGCTGGCTCAGTATGGTACAGTAGAGAACTGTGAGCAAGTGAACACCGAGAGTGAGACGG
                                                                                                                                                                                                                                                                                          rgAlaArgGlnIleAlaAlaBysIleGlyGlyAspAlaAlaThrThrValAsnAsnT
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                                                                                                                                                                                                                                    -GlyProGlyGlyGlyGlyAlaSerGlyGlyProSerGl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 256 hrlleLysGlnLeuGlnGluArgAlaGlyValLysMetlleLeulleGlnAspGlySerG
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                             GlyProProProProAlaGlyGlyGlyGlyGlyAlaAla-
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                                                                                                                                                                                                                                                                                                                                                                                                       376 GAGGGGCTTTGGCTCTCGGGGTCAGCCCCGCCAG-
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                                                                                              Alagly-GlyGlyPropro-
                                                                                                                                                                   41 yGlyGlyGly----
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ò	1299	AACTICTITGGICCCAAGGAGGAGGIGAAGCIGGAGACCCACAIACGIGIGCCAGCAICA 1358
qq	367	<pre>trpasnMetGlyProProGlyGlyLeuGlnGluPheAsnPhelleValProThrGly 385</pre>
οy	1359	GCAGCTGGCCGGGTCATTGGCAAAGGTGGAAAAACGGTGAACGAGTTGCAGAATTTGACG 1418
qq	386	LysThrGlyLeuileileGlyLysGlyGlyGluThrileLysSerileSerGlnGlnSer 405
δy	1419	
QQ	406	4
δ	1476	GTGABABATCATCGGACATTTCTATGCCGGTCGGATGGCTCAGAGGAG 1523
qq	426	PheThrileArgGlyThrProGlnGlnIleAspTyrAlaArgGlnLeuileGluGluLys 445
δλ	1524	ATCGAGACATCCTGGCCCAGGTTAAGCAGCAGCATCAGAAGGACAGAG 1573
qq	446	IleGlyGlyProValAsnProLeuGlyProProValProHisGlyProHisGlyVal 464
ζ	1574	TAACCAGGCCCAGGCACGGA 1611
q	465	ы
δ	1612	CCTGTCCCTTNGAGTCCAGGA 1632
qa	483	oProGlyPro
ò	1633	CAACAACGGGCAGAAATCG 1651
qu	503	roTyrAlaProGlnGlyTrpGlyAsnAlaTyrProHisTrpGlnGlnGlnAlaProProA 523
ŏ	1652	CTCTCCCCGGCAGGCCTGAGAATGAGTGGGAATCCGGGACACNTGGGCCGGG 17
Ор	523	:: spproalalysAlaGlyThrAspProAsnSerAla-AlaTrpAlaAla 538
ď	1712	CAGGITTGCCCACTTGATTGAGAAGATGTTCCAGTGAGGAACCCTGAT
qq	539	TyrTyrAlaHisTyrTyrGlnGlnBla548
ζ	1772	TCAGCCCAAACACCCACCCAATTGGCCCAACACTGTNTGCCCCTCGGGGTGTCAGA 1828
ą	549	GlnProProProAlaAlaProAlaGlyAlaProThrThrThrGlnThrAsnGlyGlnGly 568
ζ	1829	AATTNIAGCGCAAGGCACTTITAAACGIGGAIIGITIIAAAGAAGCICTCCAGGCCCCACC 1888
qu	569	AspGinglnAsnProAlaProAla 576
δλ	1889	19
од	577	sAl
ζ	1925	AAAITICCIICAGGI 1939
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                                                                     **Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
REDLINE=22388257; PubMed=12477932;
Retrausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Riausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Interchen M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
Raba S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunzrane P.H.,
Richards S. Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,
Villalon D.K., Wuzny D.M., Madam A., Rodrigues S., Sanchez A.,
Nhiting M., Madam A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman U.W., Green B.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.;
Menan and minital analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                        Avigan M., Levens D., "A sequence-specific, single-strand binding protein activates the far upstream element of c-myc and defines a new DNA-binding motif.";
                                                                                                                                                                                           096AE4; 012828;
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Far upstream element binding protein 1 (FUSE binding protein 1) (FBP)
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 1), SEQUENCE OF 191-193; 203-206; 72-279; 284-290; 300-314; 321-328; 394-397; 409-411; 430-438 AND FUNCTION.
TISSUE=Leukemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 45-64; 133-145; 271-283; 308-321; 379-386; 414-424 AND
                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                               Duncan R., Bazar L., Michelotti G., Tomonaga T., Krutzsch H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vindigni A., Ochem A., Triolo G., Falaschi A., "Identification of human DNA helicase V with the far upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                        1873 CTCTCCAGGCCCCACCAAGAGGGTGGATCACACC--
                                                                                                        1909 AGTGGGAAGAAAATAAAATTTCCTTCAGGT 1939
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588 sMetGlyGlnAlaValProAlaProAlaGly 598
                               560 nThrAsnĠİyGlnGlyAspGlnGlnAİa-----
                                                                                                                                                                                    643 AA.
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MEDLINE=22166132; PubMed=12176931;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res. 29:1061-1067(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21127960; PubMed=11222755;
                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=94170991; PubMed=8125259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genes Dev. 8:465-480(1994).
                                                                                                                                                                                                                                                         (DNA helicase V) (HDH V).
                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           binding protein.
                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- FUNCTION: Regulates MYC expression by binding to a single-stranded far-upstream element (FUSE) upstream of the MYC promoter. May act both as activator and repressor of transcription.
-!- SUBGNIT: Interacts with SIAHBPI/FIR and JTV1.
-!- SUBCELLULAR LOCATION: Nuclear (Probable).
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRUCTURE BY NMR OF 278-447 IN COMPLEX WITH SINGLE STRANDED FUSE DNA. MEDLINE-2184720; PubMed=11875576;
Braddock D.T., Louis J.M., Baber J.L., Levens D., Clore G.M.;
"Structure and dynamics of KH domains from FBP bound to
                                                                                                                                                                                                                                                                                                                                                                                                   DEGRADATION.
MEDILTRE=22716800; PubMed=12819782;
Kim M.J., Park J.-H., Kang Y.-S., Kim H.J., Park J.-H., Kang J.W.,
Lee S.W., Han J.M., Lee H.-W., Kim S.;
"Downregulation of FUGE-binding protein and c-myc by tRNA synthetase
cofactor p38 is required for lung cell differentiation.";
Nat. Genet. 34:330-336(2003).
                                                                                                                                                                                                                                                    interacting repressor targets TFIIH to inhibit activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KH 1.
KH 2.
KH 3.
KH 4.
GLY-RICH.
GJY-RICH.
RAC-RICH.
GQ -> CRFDPASIELAL (in isoform 2).
                                                                                                                                                     MEDLINE=20337922; PubMed=10882074;
Liu J., He L., Collins I., Ge H., Libutti D., Li J., Egly J.-M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note=No experimental confirmation available, PTM: Ubiquitinated. This targets the protein for proteasome-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00322; KH; 4.
PROSITE; PS50084; KH TYPE_1; 4.
Transcription regulation; Trans-acting factor; Nuclear protein; DNA-binding; Repeat; Ubl conjugation; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                      INTERACTION WITH JTV1, UBIQUITINATION, AND PROTEASOME-MEDIATED
Rappsilber J., Ryder U., Lamond A.I., Mann M.;
"Large-scale proteomic analysis of the human spliceosome.";
Genome Res. 12:1231-1245(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=Q96AE4-2; Sequence=VSP 008321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=Q96AE4-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -! - SIMILARITY: Contains 4 KH domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR008160; Collagen.
InterPro; IPR004087; KH dom.
InterPro; IPR004088; KH-type_1.
Pfam; PF00013; KH; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single-stranded DNA.";
Nature 415:1051-1056(2002)
                                                                                                                                                                                                                                                                                                          Mol. Cell 5:331-341(2000)
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                                                                                                                     INTERACTION WITH SIAHBP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PDB; 1J4W; 06-MAR-02.
Genew; HGNC:4004; FUBP1.
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                                                                                                                                                                                                                       Levens D.;
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2). /FIId=VSP_008322. CONFLICT 93 93 MISSING (IN REF. 2). SEQUENCE 651 AA; 68539 MW; F4EECA62FD9FA0D5 CRC64;	t Scores: 2.81e-08 .: 251.00 Similarity: 35.06 al Similarity: 7.118 tch: 1	3-270-437D-7 (1-1946) x FUB1_MOUSE (1-651)	134 TATTCCACCCCAGCTCCGATGGGAAGTACTGGACAGCCTGCTGGCTCAGTATGG 187	188 TACAGTAGAGAACTGTGAGCAAGTGAACACCGAGAGTGAGAGGGGAGTGGATGTCAC 247	21Gly-ValValAspAl 26	248 CIAITCCAACCGGGAGCAGACCAGGCAAGCCATCATGAAGCTGAATGGCCACCAGTT 304	CCTGA	45AlaGlyThrSerLe 49	365 GAATGGGCGCCGAGGGGCTTTGGCTCTCGGGGTCAG	 49 uAsnSerAsnAspTyrGlyTyrGlyGlnLysArgProLeuGluAspGlyAspGlnPr 69	402	69 oAspAlaLysLysValProProGlnAsnAspSerPheGlyAlaGlnLeuProProMetHi 89	(b)	9 sGinGinserArgservaimetiniGiuGiulyiLysvairiOAspGiymetvaiGi 10	497 TGCCATTATTGGCAAGGAGCCACCATCCGCAACATCACAAAACAAAC	GATAGACGTGCATAGGAAGGAGGAACGCAGGTGCAGGTGAAAAAGCCATCAGTGTGCACTC 61	::: ::: ::: 129 slleGlnlleAlaProAspSerGlyGlyLeuProGluArgSerCysMetLeuThrGl 148	617 CACCCCTGAGGGCTGCTCCTCGGTTGTAAGATGATCTTGGAGATTATGCATAAA 671	72 -GAGGCTAAGGACACCAAAACGGCTGACGAGGTTCCCCTGAAGATCCT	 ::: ::: 168 gProAlaProGlyPheHisHisGlyAspGlyProGlyAsnAlaValGlnGluIleMetII 188	722 CCATAATAACTTTGTAGGGGGTCTCATTGGCAAGGAAGGA	:::	AAGATACCGAGACAAAATCACCATCTCCTCGTT	208 nGluArgAlaGlyValLySMetValMetIleGlnAspGlyPr 222	! ! !	222 oGlnAsnThrGlyAlaAspLysProLeuArglleThrGlyAspProTyrLysValGlnGl 242	887 GGCCGAGCAGCAGTAATGAAGAAATTCGGGAG
FT FT SQ	Alignmen Pred. No Score: Percent Best Loc Query Ma DB:	US-09	λ δ	δ	qq	ð	a ò	- q	δ	qq	δλ	οg	\d	Q T	ð A	ò	qq	δy 83	λõ	đ	δλ	qq	ò	qq	ò	qq	ò

242	nAlaLysGluMetValLeuGluLeuIleArgAspGlnGlyGlyPheArgGluValArgAs 262
932	GATGTGGCTGCCATGAGCTCTCACCTGATCCCTGGACCTGAACCTGGCTGCTGTAGGTCT 991
262	: : : nGluTyrGly 265
992	TITCCCAGCTICATCCAGCGCAGTCCCGCCGCCTCCCAGCGGTTACTGGGGCTGCTCC 1051
266	270
1052	TCCCGAGCAGAGATGGTGCAGGTGTTTATCCCGGCCA
271	h 281
1112	GGCAGTGGGCGCCATCATCGGCAAGAAGGGGCAGCACATCAAACAGCTCTCCCGGTTTGC 1171 ::: ::
301	CAGCGCCTCCATCAAGATTGCACCACCCGAAACACCTGACTCCAAAGTTCGTAT 1225
1226	GGTTATCATCACTGGACCGCCAGAGGCCCAATTCAAGGCTCAG
1269	GGAAGAATCTATGG 1282
338	uLeuArgSerValGlnAlaGlyAsnProGlyGlyProGlyProGlyAlyArgGlyArgGl 358
1283 358	CAAACTCAAGGAGGAGAACTTCTTTGGTCCCAAGGAGGAAGTGAAGCTGGAGACCCACAT 1342 ::: ::: ::: ::: ::: ::: yArgGlyGlnGlyAsnTrpAsnMetGlyProProGlyGlyLeuGlnGluPheAsnPh 377
1343	ACGIGIGCCAGCATCAGCAGCTGGCCGGGTCATTGGCAAAAGGGTGGAACGA 1402 ellevalProThrGlyLysThrGlyLeullelleGlyLysGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyG
1403	GTTGCAGAATTTGACGGCAGCTGAGGTGGTAGTACCAAGAGCCCAGACCCCTGATGAGAA 1462 :::
1463	
1508	GATGGCTCAACGGAAGATCCGAGACATCCTGGCCCAGGTTAAGCAGCAGC 1557
1558	ATCAGAAGGACAGAGTAACCAGGCCCAGGCACGGAGGAAGTGAC 1602 **DPCAH'sG1\NJa1
1603	CAGCCCCTC
475	ThrProMetGlyProTyrAsnProAlaProTyrAsnProGlyProProGlyProAlaPro 494
1633	His GlubroproAlaproTurklaproGlnGluTroGluAsnAlaTurproHisTroGlu 514
1636	CAACGGCAGAAATCGAGAGTGTGCTCTCCCGGCAGGCCTGAGAATGAGTGC :: SinAlaProproAspProAlaLysAlaGlyAlaSpPr
1696	
2 2	GAGGAACCCTGATCTNTCAGCCCCAAACACCCCAATTGGCCCAACACTGTNTGC 18
546	

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1419 GCAGCTGAGGTGGTAGTACCAAGAGACCAGACCCCTGATGAGAACGACCAGGTCATCGTG 1478
                                                                                                                                                                                                                                                                              ----GGACAGAGTAACCAGGCCCAGGCACGGAGGAAGTGACCAGCCCCT 1610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1695
                                                                                                                                                                                                                                                                                                                                                                     1611 CCCTGTCCCTINGAGTCCAGGACAACAACGGGCAGAAATCGAGAGTGTGCGTCTCCCCCGGC 1670
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A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Brocheton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Bosak S.A., McKwan P.J., McKernan K.J., Malek J.A., Gunzarane P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Hallon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Halton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

B. Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

R. Generation and initial analysis of more than 15,000 full-length
                                                                                                                        444
                                                                                                                                                                                                                                                                                                                                                                                                                        464
                                                                                                                                                                                                                              412 GlndinIleGluValAlaArgdinLeuIleAspGluLysValGlyGlyThrAsnLeuGly 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        484 uThrGlnGlyTrpGlySerThrTyrGlnAlaTrpGlnGln-----ProThrGlnGlnVa 502
                                                                                                                                                                                                                                                                                                                                                                                                    1479 AAAATCATCGGACATTTCTATGCCAGTCAGATGGCTCAACGGAAGATCCGAGACATCCTG
                                                                                                                                                                                                                                                                                                                                   --Pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            464 tAlaAlaLysValAsnGlyAsnProHisSerThrProValSerGlyProProAlaPheLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUB1 MOUSE STANDARD; PRT; 651 AA.
Q91WGB; Q8COX8;
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Far upstream element binding protein 1 (FUSE binding protein 1) (PBP).
FUBPI OR DESETEDSORE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1743 AAGAIGITCCAGIGAGGAACCCIGAICINTCAGCCCCAAACACCCCAATIGG 1797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                502 lProserGlnGlnSerGlnProGlnSerSerGlnProAsnTyrSerLysAlaTrp 520
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                        ||| ||| ::: ::: |||::: ||| 385 GlyAlaHisValGluLeuGlnArgAsnProProProAsnSerAsp------
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                                                                                                                                                                                                                                                                                                           432 AlaProGlyAlaPheGlyGlnSerProPheSerGln-
                                                                                                                                                                                  1539 GCCCAGGTTAAGCAGCAGCATCAGAAG----
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STRAIN=C57BL/6J; TISSUE=Head;
MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1671 AGGCCTGAGAATGAGTGGGAATCCG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human and mouse cDNA sequences.
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RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C.,

Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Schriml L.M., Ranapin A., Matsuda H., Batalov S., Beisel K.W.,

Balde J.A., Brade D., Brusic C., Chothia C., Corbani L.E., Cousins S.,

RA Gasterland T., Cariboldi M., Gissi C., Godzik A., Gough J.,

RA Gasterland T., Kawasawa Y., Kedzierski R.M., King B.L.,

RA Kanajaya A., Kurochkin I.V., Lee Y., Lehhard B. Lyons P.A.,

RA Kanajaya A., Kurochkin I.V., Lee Y., Lehhard B. Lyons P.A.,

RA Maglott D.R., Maltais L., Marchiomni L., McKenzie L., Miki H.,

RA Bayashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

RA Asadelin A., Schneider C., Semple C.A., Setou M.J., Shimada K.,

Sultana T., Mynshawa T., Rompo H., Rangide R.D., Tomita M.,

Verardo R., Wagner L., Wahlestedt C., Wang Y., Matanbe Y., Wang L.,

Wilming L.G., Wynshawa Boris A., Carainci P., Hayatsu N.,

Hirozane-Kibhikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,

RA Milanig L.G., Wang K., Kawai J., Aizawa K., Shinagawa T., Fukuda S.,

Hara A., Hashizume W., Imchari K., Ishii Y., Itoh M., Kagawa I.,

Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,

Birney B., Hayashizaki Y.,

Nature 420:563-573(2002).

Hature 420:563-573(2002).

Ra Lugaraki A. Sasaki D., Shibata K., Shinagawa A.,

Nature 420:563-573(2002).

Hature 420:563-573(2002).

Subunin Interacts with SIAHBPI/FIR My atmilarity).

Haranya Ra activator and repressor of transcription (By similarity).

Haranya Randelman (Probable).

Haranya Randelman (Probable).

Haranya Randelman Randelman (Probable).

Haranya Randelman Randelman (Probable).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note=No experimental confirmation available;
-!- PTM: Ubiquitinated. This targets the protein for proteasomemediated degratation (By similarity).
-!- SIMILARITY: Contains 4 KH domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWART; SM00322; KH; *.

PROSITE; PS50084; KH TYPE 1; 4.

Transcription regulation; Trans-acting factor; Nuclear protein; DNA-binding; Repeat, Ubl conjugation; Alternative splicing.

DOMAIN 181 247 KH 1.

DOMAIN 271 335 KH 1.

DOMAIN 372 439 KH 4.

DOMAIN 372 439 PIOY-GLY.

DOMAIN 446 556 PRO-RICH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=Q91WJ8-1; Sequence=Displayed;
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MGD; MGI:1924642; 9530027K12Rik.
InterPro; IPR008160; Collagen.
InterPro; IPR004087; KH dom.
InterPro; IPR004088; KH_Lype_1.
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SMART; SM00322; KH; 4.
                      HARREN BERREN BE
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-- DGSWTNPSSTTHWEGMPSPFKD (in isoform

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GAG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCTCTCGGGGGTCAGCCC---CGCCAGGGCTCACCTGTGGCAGCGGGGGCCCCCAGCCAAG 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----CACCAGIIGGAGAACCAIGCCCIGAAGGIC 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     327 TCCTACATCCCCGATGAGCAGATAGCACAGGGACCTGAGAATGGGCGCCGAGGGGTTT 386
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54 GlyValGlnLysArgProLeuAspAspGlyValGlyAsnGlnLeuGlyAlaLeuValHis 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 MetLysAlaGluGlyPheValAspAlaLeuHisArgValArgGlnIleAlaAlaLysIle 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 AspSerileProHisLeuAsnAsnSerThrProLeuValAspProSerValTyrGlyTyr 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00322; kn; J.

PROSITE; PS500B4; KH TYPE 1; 4.

Transcription regulation; Trans-acting factor; Nuclear protein;

DNA-binding; Repeat; Alternative splicing.

TO 141 KH 1.

DOMAIN 162 228 KH 2.

DOMAIN 253 317 KH 3.

DOMAIN 354 421 KH 3.

DOMAIN 354 421 KH 4.

VARSPLIC 1 64 MABIVGQSAPVGMKAEGFVDALHRVRQIAAKIDSIPHLNN

STRUNDBSVYGYGVQKRPLDDGV -> MPPI (in
                                                                                                                                                                                                                                                                                                                                                        CAUTION: Ref.2 (AAH01325) sequence differs from that shown due to a frameshift in position 527.
       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
-!- FUNCTION: May interact with single-stranded DNA from the far-
upstream element (FUSE). May activate gene expression.
-!- SUBCELLULAR LOCATION: Nuclear (Probable).
                                                                                                                                                                                                                                                                                                             CAUTION: Ref.1 sequence differs from that shown due to a
                                                                                                                                                                                                                                           Note=No experimental confirmation available,
TISSUE SPECIFICITY: Detected in a number of cell lines.
SIMILARITY: Contains 4 KH domains.
                                                                                                                                                                                                                        VSP 008324;
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TId=VSP 008324.

-> D (IN REF. 1).

FIBE223542BC197D CRC64;
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126
90
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218
                                                                                                                                    Event=Alternative splicing; Named isoforms=2;
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                        IsoId=096I24-2; Sequence=VSP_008323,
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                                                                                                                                                                              IsoId=Q96I24-1; Sequence=Displayed;
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EMBL; BC001235; AAH0135.1; ALT_FRAME.
EMBL; BC007874; AAH07874.1; -.
Genew; HGNC:4005; FUBP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR004087; KH dom.
InterPro; IPR004088; KH type_1.
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SMART; SM00322; KH; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ::: |||::::::|||
113 Ile---AlaSerGluSerSerGlyIleProGluArgProCysValLeuThrGlyThrPro
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206 ThrGlyAlaAspLysProLeuArgIleThrGlyAspAlaPheLysValGlnGlnAlaArg
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                                                                             ATTGGCAAGGAGGGGCCACCATCCGCAACATCACAAAACAGACCCAGTCCAAGATAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----CATAAAGAGGCTAAGGACACCAAAACGGCTGACGAGGTTCCCCTGAAGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          152 ProGlyPheHisAsnAspIleAspSerAsnSerThrIleGlnGlu
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REQUENCE FROM N.A. (ISOFORMS 1 AND 2).

REQUENCE FROM N.A. (ISOFORMS 1 AND 2).

REDILNEL-238825; PubMed-12477932;

REDILNEL-238825; PubMed-12477932;

REDILNEL-238825; PubMed-12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Scheefer C.R., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Scheefer G.D.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Mang J., Hsieh F.,

RA Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Distchenko L., Marusina K., Forninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RIGHARD D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rhiting M., Madan A., Young A.C., Schwchenko Y., Bouffard G.G.,

Rhiting M., Madan A., Young A.C., Schwchtz J., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Marza M.A.,

Rotherfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rohertion and initial analysis of more than 15,000 full-length
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triticum ae
homo sapien
                                                                     oryctolagus
mus musculu
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homo sapien
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MEDLINE=97094955; PubMed=8940189;

Davis-Smyth T., Duncan R.C., Zheng T., Michelotti G., Levens D.;

"The far upstream element-binding proteins comprise an ancient family of single-strand DNA-binding transactivators.";

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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
MCBI_TaxID=9606;
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ID FUB3 HUMAN STANDARD;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

PR Par upstream element binding protein 3 (FUSE binding protein 3).
                   Q15366 P
Q07244 P
O19049 c
Q61990 r
P38151 P
P06105 P
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P10387
Q96dn6
P10388
Q9p2p6
Q8in94
P78559
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P97609
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S160 YEAST
YBD2 YEAST
YDRH HUMAN
YAV2 XANCV
GLT0 WHEAT
                                                                                                                                                                                                                                                          MBD6 HUMAN
GLT5 WHEAT
STR9 HUMAN
OSA DROME
                                                                                                                                                                                                                                                                                                                                     OSA DROME
MAPA HUMAN
GLT4 WHEAT
BAT2 HUMAN
IE18 PRVIF
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PCLO HUMAN
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  Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-Q=/cgn2 1/USF0 spool py/USG9270437/runat 23072004 095739 27413/app query.fasta_1.5582
-Q=/cgn2 1/USF0 spool py/USG9270437/runat 23072004 095739 27413/app query.fasta_1.5582
-D=SwissProt_42-OFWT=fastan -SUFFIX=rsp-MINMATCH=0.1 -LGOPCL=0 -LGOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LLST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE-LOCAL
-UOTFMT=pcto -NORM=ext -HEADFSIZES=500 -MINLEN=0 -MAXLENE-2000000000
-USER=USG9270437 acGn 1 1 57 @runat 23072004 095739 27413 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELDEXT=7
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                                                 Compugen Ltd.
                                                                                                                    OM nucleic - protein search, using frame plus n2p model
                        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compug
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2 Gaps: 13 0-437D-7 (1-1946) x S41224 (1-396)	459 ATCCCCCTTCGGCTCCTGGTGCCCAGTATGTGGGTGCCATTATTGGCAAGGAGGGG 518 ::: :::	579 AACGCAGGTGCAGCTGAAAAAGCCATCAGTGCACTCCACCCCTGAGGGCTGCTCCTCC 638 :::::		TGTTGCAGGGCCGAAATAATGAAAATTCGGGAGGCCTATGAATGTG TGTTGCAGGGCCCGAAATAATGAAAATTCGGGAGGCCTATGAATGTG TGTTGCAGGGCCCATGAATGATGTG	ThrMetMetPheAspAspArgArgGlyArgProHisGlyPheSerMetHisAlaArgGly 22 CTTTTCCCAGCTTCATCCAGCGCAGTCCCGCCCTCCCAGCGTTACTGGGGCTGCT 10 GlyPhe	III
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Search completed: July 23, 2004, 11:17:47 Job time: 54.4003 secs

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C;Species: Xenopus laevis (African clawed frog)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 20-Jun-2000
C;Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 20-Jun-2000
C;Accession: $41224
R;Siomi, H.; Matunis, M.J.; Michael, W.M.; Dreyfuss, G.
Nucleic Acids Res 21, 1193-1198, 1993
A;Title: The pre-mRNA binding K protein contains a novel evolutionarily cons A;Title: The pre-mRNA binding K protein contains a novel evolutionarily cons A;Reference number: $41224
A;Reference number: $41224
A;Residues: 1-396 <$10>
C;Superfamily: transformation upregulated nuclear protein HNRPK
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                              690 PheProValGluGlySerGlySerAspThr-----ValVallleArgGlyProSerSer
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                                                                                                               -----SerIleGlnLysAspLeuAla
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 24-Sep-1999
C;Accession: A44125
R;McKnight, G.L.; Reasoner, J.; Gilbert, T.; Sundquist, K.O.; Hokland, B.; McKernan, P.;
A;Title: Chem. 267, 1213-12141, 1992
A;Title: Cloning and expression of a cellular high density lipoprotein-binding protein R;Reference number: A44125, MUID:92291094, PMID:1318310
A;Accession: A44125
A;Accession: A44125
A;Status: pre-liminary
A;Residues: 1-1268 -MCK>
A;Residues: 1-1268 -MCK>
A;Residues: 1-1268 -MCK>
A;Residues: Careferences: GB:M64098; GB:M83789; NID:g183891; PIDN:AAA35962.1; PID:g183892
C;Superfamily: vigilin
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463 AspGlnTyrLysValSerValArgIleProProAspSerGluLysSerAsnLeuIleArg 482
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158 CysValLysGlnIleCysLeuValMetLeuGluThrLeuSerGlnSerProGlnGlyArg 177
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LeuProAsnSerThrGluArgAlaIleThrIleAlaGlyValProGlnSerValThrGlu 157
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                                       CAGTATGTGGGTGCCATTATTGGCAAGGAGGGGCCACCATCCGCAACATCACAAAACAG 545
                                                                                                                      546 ACCCAGTCCAAGATAGACGTGCATAGGAAAGGAGAACGCAGGTGCAGCTGAAAAAGCCATC 605
                                                                                                                                                                                                   606 AGTGTGCACTCCACCCTGAGGCTGCTCCTCCGCTTGTAAGATGATCTTGGAGATTATG 665
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ThrLeuThrGlyProThrAsnAlaIlePheLysAlaPheAlaMetIleIleAspLysLeu 79
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                                                            -SerGluGlyAsnCysProGluArgllelle
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A44125
high density lipoprotein-binding protein, 110K - human
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                                                                                                                                             serGlyAlaArglleAsnIle---
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A; Cross-references: EMBL:X78137; NID:g460770; PIDN:CAA55016.1; PID:g460771
A; Cross-references: EMBL:X78137; NID:g460770; PIDN:CAA55016.1; PID:g460771
A; Cross-references: EMBL:X78137; NID:g460770; PIDN:CAA55016.1; PID:g460771
A; Note: submitted to the EMBL: Grant formed harch 1994
B; Aasheim, H.C.; Loukianova, T.; Deggerdal, A.; Smeland, E.B.
A; Assheim, H.C.; Loukianova, T.; Deggerdal, A.; Smeland, E.B.
A; Title: Tissue specific expression and cDNA structure of a human transcript encoding a A; Reference number: S43489; MUID:94203810; PMID:8152927
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NyAlternate names: nucleic acid-binding protein; protein PCBP-1
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Feb-1996 #sequence revision 01-Mar-1996 #text change 01-Dec-2000
Cispecies: S58529; S58523; $65678; S43489; S41378; S42472
Rikiledjian, M.; Wang, X.; Liebhaber, S.A.
EMBO J. 14, 4357-4364, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Identification of two KH domain proteins in the alpha-globin mRNP A;Reference number: S58523; MUID:96016208; PMID:7556077 A;Accession: S58529
                                                                                                                            TITIGGTCCCAAGGAGGAAGTGAAGCTGGAGACCCACATACGTGTGCCAGCATCAGCAGCT
                                               ----IleAlaValProGluAsnLeuVal
                                                                                                     GGCCGGGTCATTGGCAAAGGTGGAAAAACGGTGAACGAGTTGCAGAATTTGACGGCAGCT
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C;Genetics:
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Matches:
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Indels:
                                             421 AspGlySerLysAspValValGlu----
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A Molecule type: protein
A Residues: 125-139,251-265,315-323 <KIZ>
R Leffers. H.; Dejgaard, K.; Celis, J.E.
Eur. J. Biochem. 230, 447-453, 1995
A, Title: Characterisation of two major cel
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A;Molecule type: mRNA
A;Residues: 1-298,'H' <AAS>
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A;Molecule type: protein
A;Residues: 1-356 <KIL>
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C; Keywords: RNA binding
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	1764 CTGATCTNTCAGCCCCAACACCCAC	Oy 1824	RESULT 12 138489 onconeural ventral antigen-1 - human C;Species: Homo sapiens (man) C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 05-Nov-1999 C;Accession: 138489	K; Buckanoviol, K.U.; Posner, J.B.; Darnell, K.E. Neuron 11, 657-672, 1993 A;Title: Nova, the Paraneoplastic Ri Antigen, is Homologous to an RNA-Binding Protein A;Reference number: 138489; MUID:94000830; PMID:8398153 A;Accession: 138489; MUID:94000830; PMID:8398153 A;Accession: 138489; translated from GB/EMBL/DDBJ A;Rocelle type: mRNA A;Rocelle type: mRNA A;Cross-references: EMBL:U04840; NID:g440877; PIDN:AAA16022.1; PID:g440878 C;Genetics:	Alignment Scores: 1.75e-07 Length: 510 Pred. No.: 221.50 Matches: 111 Percent Similarity: 34.89% Conservative: 68 Best Local Similarity: 21.64% Mismatches: 173 Query Match: 6.27% Indels: 161 DB: 2 Gaps: 17	US-09-270-437D-7 (1-1946) x 138489 (1-510) QY

579 AACGCAGGTGCAGAAAAAGCCATCAGTGCACTCCACCCCTGAGGGCTGCTCCTCC 638 110 Asprosersininininininininininininininininininin	170	TCCAGCGCAGTCCCGCCGCCT ATGCAGGCTCCCGAGCAGAG ATCATCGGCAAGAAGGGGCAG ATCATCGGCAAGAAGGGGCAG ATCATCGGCAAGAAGGGGCAG ATCATCGGCAAGAAGGGGCAG	CGGTTTGCCAGCGCCTCCAAGATTGCACCACCCGAAACACTGACTCCAAGGTTCGT MetGluThrdlyThrLysileGlnPheLysProAspAspAspProSerThrProGluArg ATGGTTATCATCACTGCACGCCAGAGGCCCAATTCAAGGCTCAGGGAAGAATCTATGGC :::	316 LeuValLysLysSerThrMetGlnGlnGlyGlyGlyGlyAsnValAlaGlyAlaMetVal 335 1320 GAAGTGAGGAGCCCACATACGTGTGCCACCATCAGCAGCTGGCCGGGTCATT 1376 :::	CCAAGAGCCCAGATCAGAACGACCAGGTCATCGTG
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	1764 CTGATCTNTCAGCCCCAAACCCAC	Oy 1863 TTTAAAGAGCCTCCACCAAGAGGTGGATCACACCTCAG 1910 bb 546	A; Reference number: Z19092 A; Accession: T19217 A; Accession: T19217 A; Accession: T19217 A; Molecule type: DNA A; Residues: 1-611 < WIL> A; Cross-references: EMBL:Z73969; PIDN:CAA98233.1; GSPDB:GN00023; CESP:C12D8.1b A; Experimental source: clone C12D8 A; Genetics: C; Genetics: A; Genetics: A; Map position: 5 A; Introns: 181/3; 340/3; 535/2	3.41e-08 23.00 23.2.00 37.15% arity: 18.75%	US-09-270-437D-7 (1-1946) x T19217 (1-611) QY

AlaSerGlyTyrGlyGlnAlaGlyGlnGlyTyrGlnGlnAspGlyTyrGlyAla GCCAGCATCAGCAGCGGGTCATTGGCAAAGGGGAAAAACGGTGAACGAGTTGCA :::	8 % B	579 AACGCAGGTGCAAAAAGCCATCAGTGTGCACTCCACCCCTGAGGGCTGCTCCTCC 638 ::: ::: :::::::::::::::::::::::::::::
1409 GAATTTGACGGCAGCTGAGGTGGTAGTACCAAGAGCCAGACCCTGATGAGAACGA 1465 1::	Qy	
	දු පු	747 ATTGGCAAGGAAGGAACCTGAAGAAGGTAGAGCAAGATACCGAGACAAAAATGCC 806
	ර <u>අ</u>	807 ATCTCCTCGTTGCAAGACCTTACCCTTTACAACCCTGAGAGGACCATCACTGTGAAG 863 ::: ::: :::::::::::::::::::::::
1586 GGCACGGAGGAAGCCAACCCCCCCCCTCTNGAGTCCAGGACAACAACGGCAG 1645 11:::: 490 rThrGlyGlnGlnProProAlaGlnGlySerThrGlyGlnAlaGlyTyrGlyAlaProPr 510	oy G	864 GGGGCCATCGAGAATTGTTGCAGGGCCGAGCAGGAAATAATGAAGAAAGTTCGGGAGGCC 923
1646 AAATCGAGAGTGTGCTCCCCGGCAGGCCTGAGAATGAGTGGGGAATCCGGGACACNTGG 1705 ::: 510 oThrSerGlnAlaGlyTyrSerSerGlnProAlaAlaAlaTyrAsnSerGlyTyrGlyAl 530	} & ;	TATGAGAATGATGTGGCCATGAGCTCTCACCTGATCCCTGAACCTGGCTGCT
1706 GCCGGGCTGTAGATCAGGTTTGCCCACT 1733 	G & E	GIAGGICTTTCCCAGCTTCATCCAGCGCAGTCCCGCCGCCGCCCCCAGCAGCGTTACTGGG
al protein C12D8.1a - Caenorhabditis elegans Caenorhabditis elegans	3 8 8	CCCIATAGCTCCTTTATGCAGGCTCCCGAGCAGGAGATGGTGCAGGTGTTTATC . ::
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T19216 R;McMurray, A. submitted to the EMBL Data Library, June 1996	<i>장</i> 셤	1104 CCCGCCCAGGCAGTGGGCGTCATCATCGGCAAGAGGGCAGCACATCAAACAGCTCTCC 1163
<pre>i number: 219092 i: T19216 vreliminary; translated from GB/EMBL/DDBJ trpe: DNA</pre>	상 업	1164 CGGTTTGCCAGCGCCTCCATCAAGATTGCACCACCCGAAACACCTGACTCCAAAGTTCGT 1223 1164 CGGTTTGCCAGCGCCTCCATCAAGATTGCACCCCGAAACACCTGACTCCAAAGTTCGT 1223 1164 CGGTTTGCCAGCACACCAAAGAAGAACACCGAAACACTGAAGAAGAACACTGAAACAAAAGAAAG
A;Residues: 1-589 <wil> A;Resisterses: 1-589 <wil> A;Cross-references: BMBL:Z73969; PIDN:CAA98232.1; GSPDB:GN00023; CESP:C12D8.1a A;Experimental source: clone C12D8 C;Genetics:</wil></wil>	\$ A	1224 ATGGTTATCATCACTGGACGCCCAGATTCAAGGCTCAGGGAAGAATCTATGGC 1283
sp:C12DB.la idon: 5 7/3; 25/1; 159/3; 318/3; 513/2	ζ. Oy	1284 AAACTCAAGGAGGAGAACTTCTTGGTCCCAAGGAG 1319
3.37e-08 232.00 37.15%	\delta	1320 GAAGTGAAGCTGGAGACCCACATACGTGTGCCAGCATCAGCAGCTGGCCGGGTCATT 1376 114 SerAsnGluAlaSerThrPheTyrMetSerValProAlaAlaLysCysGlyLeuVallle 333
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1	Qy Dp	1437 CCAAGAGACCAGACCCCTGATGAGAACGACCAGGTCATCGTGAAA 1481 ::: :::::: 354 SerArgAspProThrGlyAsnAlaAspGluLysVall1eLysGlyGlyGlyLysArg 373
ProAlaLysArgProAlaAspAspThrAspLeuAsnProPheMetAspAspAsnGluAlaCGGCTCCTGGTGCCCACCAGTATGTGGCATTATTGCAAGGAGGG ::: :: :::	% qa	1482 ATCATCGGACATTICTATGCCAGTCAGAGGCTCAACGGAAGATCCGAGACATCCTGGCC 1541
48 ValasnGluLysTyrProIleProGluSerAlaValGlyIleValIleGlyArgGlyGly 67 519 GCCACCATCGGCAACATCACAAAACAGCCCAGTCCAAGATAGACGTGCATAGGAAGGA	ठे १	1542 CAGGTTAAGCAGCATCAGAAGGGACAGGGTAACCAGGCCCAGGCACGGAGGAAGTGA 1601
::: ::: 68 SerGlulleGlnGlyileGlnAlaLysAlaGlyCysArgValGlnMetSerProAspAla 87	g &	SAGAGTGTGCT

347 GATAGCACAGGGACCTGAGAATGGCGCCGAGGGGGCTTTGGCTCTCGGGGTCAGCCCCG 406 ::: ::: ::		584 AGGTGCAGGTGAAAAGCCATCAGTGTGCACTCCACCCTGAGGGCTGCTCCT 637	195 sAjaGluGlnLeuijeThrAspValLeuGlnGluAlaGjùAlaGlyAsnThrAlaGlySe 215 687	713 GATCCTGGCCCATAATAACTTTGTAGGCGTCTCATTGGCAAGGAAGG	773 GAAGGTAGAGCAAGATACCGAGACAAAATCACCATCTCCTCGTTGCAA 821	822 -GACCTTACCATTACAACCCTGAGAGCACCATCACTGAAGGGGGCCATCGAGAATTG 880 [881 TTGCAGGCCGAGCAGGAAATAATGAAGAAGTTCGGGAGGCCTATGAGAATGATGGC 940	TGCCATGAGCTCTCACCTGATCCCTGACCTGAACCTGCTGCTGTAGGTCTTTTCCCAGC ::: ::: :::	1001 TTCATCCAGCGCAGTCCCGCCGCCGCCAGGGTTACTGGGGGCTGCTCCCTATAGCTC 1060 318 nGlnGlyGlyTyrGlnAlaArgProProSerSerTrp-AlaP 332	1061 CTTTATGCAGGCTCCCGAGCAGAGAGAGGTGTGTTATCCCGGCCCAGGCAGT 1117	1118GGGGGCCATCATCGGAAAAAAAGAAGAA 1144	1145 GCACATCAAACAGCTCTCCCGGTTTGCCAGGGCCTCCATCAAGATTGCACCC 1198 :: ::: ::: 372 GlytyrTyrAepGlnSerSerValProProSerGlnGlnSer 385	1199 GGAAACACCTGACTCCAAAGTTCGTATGGTTATCAT	386AlaGlnGlyGluTyrAspTyrTyrGlyGlnGlnGlnSerGlnGlnPro 401	1235CACTGGACCGCCAGAGGCCCAATTCAAGGCTCAGGGAAGATCTATGGCAAACT 1288 [1:::	CAAGGAGGAGAACTTCTTTGGTCCCAAGGAGAAGTGAAGTGAAGACTGGAGACCACATACGTG
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1289 CAAGGAGGAGAACTTTTGGTCCCAAGGAGGAAGTGAAGCTGGAGACCCCACATACGTGT 1348

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Alignment Scores: 2.23e-08 Length: 568 Score: 234.50 Matches: 92 Percent Similarity: 42.47% Conservative: 97 Best Local Similarity: 20.67% Mismatches: 175 Query Match: 2 6.64% Indels: 16 DB: 2 Gaps: 16	-09-270-437D-7 (1-1946) x T49962 (1-568) 336 CCCGATCAGCAGATAGCACAGGGACCTGAGAATGGGCGCCGAGGGGGCTTTGGCTCTCGG 3	Db 3 ProAspHisArgMetSerProAspHisArgAspSerHisArgLySArg 18 Qy 396 GGTCAGCCCGCCAGGGTCACCTGTGGCAGGGGGCCCCAGCCAAGCAGGAGG 449 https://documents.com/argan	19 Seiaigriogimseiaspiyinapaspannsiyaiyociiysaaspisjyinisyooga 450CAAGIGGACATCCCCTTCGGCTCCTGGTCCCCACC 4	486 CAGTATOTGGGTGCCATTGGCAAGAGGGGGGCGCCATCGCCAACATCACAAAACAG 11:1 ::::::::::::::::::::::::::::::::	Qy 546 ACCCAGTCCAAGATAGACGTGCATAGGAAGGAGAACGCAGGTGCAGCTGGAAAAAGCCATC 605	OY 606 AGTGTGCACTCCACCCT	639	Qy 693 GCTGACGAGGTTCCCCTGAAGATCCTGGCCCATAATAACTTT 734	QY 735 GTAGGGGTCTCATTGGCAAGGAAGGACGGAACCTGAAGAAGGTAGAGCAAGATACCGAG 794 ::: ::::: :::: Db 158 IleGlyCysIleLeuGlyArgGlyGlyGlnIleValGInAsnIleArgSerGluThrGly 177	OY 795 ACAAAAATCACCATCTCCTCGTTGCAAGACCTTACCCTTTACAACCCTGAGG 848	OY 849 ACCATCACTGTGAAGGGGCCATCGAGAATTGTTGCAGGGCCGAGCAGGAATAATGAAG 908 Db 198 LeuileGlnileSerdlyGluValLeuIleValLySLySAlaLeuLeuGlnileAlaSer 217	QY 909 AAAGTICGGGAGCCTAIGAGAAIGAIGIGGCTGCCAIGAGCTCTCACCTGGC 968 ::::: : :::	Qy 969 CTGAACCTGGCTGTAGGTCTTTTCCCAGCTTCATCCAGCGCAGCTCCCGCCGCCTCCC 1028	OY 1029 AGCAGCGTTACTGGGGCTGCTCCCTATAGCTCC	Qy 1062TITANGCAGGCTCCCGAGGAGATGGTGCAG 1094	Qy 1095 GTGTTTATCCCCGCCCAGGCAGTGGGCGCCATCATCGGCAAGAAGGGGCCAGCACATCAAA 1154 :::
681GACACCAAAACGGCTGAGGTTCCCCTGAAGATCCTGGCCCATAATAAC	Db 253 LysCysGlyAlaileileGlyLysLysGlyGluGlnMetArgLysLeuArgSerTrpThr 272 Qy 792 GAGACAAAATCACCATCCTCGTTGCAAGACCTTACCCTTACAACCCTGAGAGGACC 851 273 AsnCysAspPheileLeuileGlnGluAsnAsnIleAlaAspSerValLysPro 290	QY 852 ATCACTGTGAAGGGGCCATCGAGAATTGTTGCAGGCCGAGCAGGAAATAATGAAGAAA 911 Db 291 LeuGln1leThrGlyGln	Qy 912 GTTCGGGAGGCCTATGAGAATGATGTGGCTGCCATGAGCTCTCACCTGATCCTGGCTG 971		Qy 1032 AGCGTTACTGGGGCTGCTCTATAGCTCCTTAATGCAGGCTCCCGAGCAGAGATGGTG 1091 ::: ::: :::!! Db 321 GlyMetalaGlyAsnSerProValalaAlaMetSerLeu 333	OY 1092 CAGGTGTTTATCCCGGCCAGGCGCGCCATCATCGGCAAGAAGGGCAGCACATC 1151 ::: :::			OY 1272 AGAATCTAIGGCAAACTCAAGGAGGAGAACTTCTIGGTCCCAAGGAGGAGGAGGAGGAGGIG 1331	0-0	Qy 1392 ACGGTGAACGAGTTGCAGAGTGACGGCGGGTGGTAGTACCAAGAGAC 1445	thaliana ess)	C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000 C;C;Accession: T49962 C;Accession: T49962 R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lesubmitted to the Protein Sequence Database, April 2000	A;Reference number: 224493 A;Acession: T49962 A;Status: preliminary A;Molecule type: DNA	A;Residues: 1-568 <bev> A;Cross-references: EMBL:AL353993; GSPDB:GN0063; ATSP:F8M21.160 A;Experimental source: cultivar Columbia; BAC clone F8M21 C;Genetics:</bev>	A;Gene: ATSP:F8M21.160 A;Map position: 5 A;Introns: 200/3; 337/3; 544/3

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GGCAAAGGTGGAAAAACGGTGAACGAGTTGCAGAATTTGACGGCAGCTGAGGTG---GTA 1433
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390 LeuGlnLysGluAspValProLysIleAlaArgGluAspGluGluMetValGlnIleThr 409
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Cipace: O6-Jan-1995 #sequence_revision O6-Jan-1995 #text_change O5-Nov-1999
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A;Accession: A53184
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A;Residues: 1-644 < DUN
A;Residues: 1-644 < DUN
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A;Molecule type: mRNA
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| ProGluArgSerCysMetLeuThrGlyThrProGluSerValGlnSerAlaLysArgLeu
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LeuAspGlnIleValGluLysGlyArgProAlaProGlyPheHisHisGlyAspGlyPro
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43	TTTCTATGCCAGTCAGATGGCTCAACGGAAGATCCGAGACATC	ài
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US-09-270-437D-7 (1-1946) x C8	1433 AGTACCAAGAGACCCCTGATGAGAACGACCAGGTCATCGTGAAAATCATCGGACA 1492	δy
Best Local Similarity: 23.75% Query Match: 7.11% DB: 2	1376 TGGCAAAGGTGGAAAAACGGTGAACGAGTTGCAGAATTTGACGGCAGCTGAGGTGGT 1432 :: ::: ::: :::	SP GS
milarity:	lLeuProGlyGlnSerIlePheTyrMetHisValProAlaGlyLysCysGlyLeuValIl	ද්ධ ,
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A;Residues: 1-479 <sto> A;Cross-references: GB:AE00517</sto>	1286 ACTCAAGGAGGAGAACTTCTTTGGTCCCAAGGAGGAAGTGAAGCTGGAGACC 1337	ζŏ
A;Status: preliminary A;Molecule type: DNA	: :::	qα
A;Reference number: A86141; MU A;Accession: C86275	1226 GGTTATCATCACTGGACCGCCAGAGGCCCAATTCAAGGCTCAGGGAAGAATCTATGGCAA 1285	ò
A; Authors: Salzberg, S.L.; Sch ker, M.; Wu, D.; Yu, G.; Frase A:Title: Sequence and analysis	1166 GTTTGCCRGCGCCTCCATCAAGATTGCACCACCGGAAACCCTGACTCCAAAGTTCGTAT 1225 478 aGluThrGlyThrLysTleGlnPheLysPcAspThrAsnProAsnScGluAspArg11 498	රු පු
A; Authors: Hunter, J.L.; Jenki C.A.; Li, J.H.; Li, Y.; Lin, X Rizzo M · Rooney T · Rowley	458 OArgLeuSerAlaGlyMetIleIleGlyLySGlyGlyGluMetIleLySArgLeuAlaAl 478	qa
Chin, C.W.; Chung, M.K.; Conr. ansen, N.F.; Hughes, B.; Huiza	707	3 8
C; Accession: C86275 R; Theologis, A.; Ecker, J.R.;	TCCCTATAGCTCCTTTATGCAGGCTCCCGAGCAGGAGATGGTGCAGGTGTTTATCCC 1	& &
hypothetical protein [imported C.Species: Arabidopsis thalian C.Pate. May 2011 #200000000000000000000000000000000	424 -GlyAsnalaProLeuLeuGlnArgalaProHisGlnProSerGlyGlnPheGlyGl 442	7 43
DD 752 LeuGlyAspValSerG	423 423	qa
-1	926 IGAGAAIGAGCTGCCATGAGCTCTCACCTGAICCCTGGCCTGAACCTGGCTGTT 985	λõ
	866 GGCQATCGAGAGATTGTTGCAGGGCCGAGCAGAATAATGAGAAAGATCGGGAGGCCTA 925 	ž 8
Db 717 AspTyrSerAlaGlnI		qu
Qy 1697 GACACNT	818 GCAAGACCTTACCCTTTACAACCCTGAGAGGACCATCACTGTGAAGGG 865	ζ
697	758 AGGACGGAACCTGAAGAAGGTAGAAGATACCGAGACAAAAATCACCATCTCCTGGTT 817 	<i>රු</i> සි
	347 yGluValThrGluGluMetLeuIleProAlaAspLysIleGlyLeuValIleGlyLysGl 367	qu
1598	698 GGAGGTTCCCCTGAAGATCCTGGCCCATAATAACTTTGTAGGGCGTCTCATTGGCAAGGA 757	δ
657	 	Db
Oy 1547 TAAGCAG	ы.	ä

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; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso nn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. zar, L.
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MUID:21016719; PMID:11130712
-- CAGCATCAGAAGGGACAGAGTAACCAGGCCCAGGCACGGAGGAA 1597
                                                                                                                                                                                                                                                                                                                                -----AGGAACCCTGATCTNTCAGCCCCAAACACCCACCCA 1792
                                                                                                                                                                 -----TCCCCGGCAGGCCTGAGAATGAGTGGGAATCCGG 1696
                                                                                                                                                                                                                                                VTGGGCCGGGCTGTAGATCAGGTTTGCCCACTTGATTGAGAAGAT 1747
                                                                             CCTGTCCCTTNGAGTCCAGGACAACAGGGCAGAAATCGAGAGTG 1657
                         |||||||
|TrpAlaAlaTyr---TyrArgSerIleGlyLeuValGluGlnAla 735
                                                                                                               ||||
| ProThrGluMetTyrGlnAsnProMetGlnGlnProGlnAlaSerV 697
                                                                                                                                                                                                                                                                                                                                                        GlnMetArgArgAsnGlnSer-----AsnThrAlaPro 751
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ana (mouse-ear cress)
e_revision 02-Mar-2001 #text_change 31-Dec-2001
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rGlyValProGln 760
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GCAGTGGGCGCCATCATCGGCAAGAAGGGGCAGCACATCAAACAGCTCTCCCGGTTTGCC 1172
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---AlaLysAsnSerThrAsnProAspGlyThrProSerAspAlaAsnThrProArgLys 180
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                                                                              AlaGiyileileilegiyLysAlaGiyLysAsnValAlaGluLeuArgSerThrThrAsn 124
                                                                                                                                                                                                                                                                                                                                                                                  828 ACCCTTTACAACCCTGAGAGGACCATCACTGTGAAGGGGGCCATCGAGAATTGTTGCAGG 887
VallysAlaGlyVal---ThrLysAlaValProAsnValHisAspArgValLeuThrIle
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|LeuArgLeuLeuIleAlaHisSerLeuMetGlySerIleIleGlyArgAsnGlyLeuArg
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292 SerGlyGluhlalleProGluAsnPheValSerTyrGlyAlaGlnValPheProAlaThr
                                                     GIGGGIGCCATTATIGGCAAGGAGGGCCCACCATCCGCAACATCACAAAACAGACCCAG
                                                                                                         TCCAAGATAGACGTGCATAGGAAGGAGAACGCAGGTGCAGCTGAAAAAGCCATCAGTGTG
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hypothetical protein ZK418.9 - Caenorhabditis elegans C;Species: Caenorhabditis elegans

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uGlyLysAsnLeuLeuTyrLysTyrGlnGlnTyrTyrSerAlaAlaLeu1leAsnHisCy 193
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eArgLeuIleGlnGlnThrSerGlyCysArgValGlnMetAspProAspHisGlnSerVa 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         153 uSerLeuLeuLeuSerAlaLeuPheLeuCysSerAlaValHisProAspIleSerThrGl 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AlallePheSerThrSerMetArgValPheAsnGluLysLysSerTyrMetHisPhePro 114
  Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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231 rLeuLysArgProLeuAsp---SerGluIleLeuAspGlyAspLeuIleProThrLysLy
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15:C;Accession: T27855
R;Fulton, L.
Submitted to the EMBL Data Library, April 1994
A;Description: The sequence of C. elegans cosmid ZK418.
A;Reference number: Z20430
A;Accession: T27855
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rocession: T27855
A;Retisence: DNA
A;Residues: 1-768 eFUL
A;Coss-references: EMBL:U00047; PIDN:AAAS0693.1; CESP:ZK418.9
A;Experimental source: strain Bristol N2
C;Genetics
C;Genetics
A;Introns: 166/1; 221/3; 243/1; 279/1; 387/3; 490/1; 567/3; 727/2
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1154
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Conservative:
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Indels:
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354

371

391

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probable pre-mRNA splicing factor - fission yeast (Schizosaccharomyces pombe) C; Species: Schizosaccharomyces pombe C; Species: Schizosaccharomyces pombe C; Species: O3-Dec-1999 #sequence_revision O3-Dec-1999 #text_change O3-Dec-1999 C; Accession: T41600
R; Puyne, M.; Rajandream, M.A.; Barrell, B.G.; Bothe, G.; Pohl, T. submitted to the EMBL Data Library, October 1998
A; Accession: T41600
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Wochelle type: DNA
A; Residues: 1-398 < LNA>
A; Residues: 1-398 < LNA>
A; Coss. references: EMBL: ALO31825; PIDN: CAA21234.1; GSPDB: GN00068; SPDB: SPCC757.09c
A; Esperimental source: strain 972h-; cosmid c757
A; Genetics:
A; Genetics:
A; Genetics: A; Genetics: A; A; And Position: 3
                                                                          ACACCTGACTCCAAAGTTCGTATGGTTATCATCACTGGACCGCCAGAGGCCCAAATTCAAG 1262
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                                  ::: ||| :::|||| 392 SerIleArgValPheAlaLysAspGlnAlaThrLysTyrGluSerGlnHisAspGluIle
                                                                                                                                                                                                                                                                                                                                                                                  GTGAAAATCATCGGACATTTCTATGCCAGTCAGATGGCTCAACGGAAGATCCGAGACATC
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412 ValGlnValIleGlyAsnLeu------LysThrValGlnAspAlaLeuPheGlnIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGGCCCAGGTTAAGCAGCAGCATCAGAAGGGACAGAGTAACCAGGCCCAGGCACGGAGG
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Mismatches:
Indels:
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27.19%
7.26%
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GluSerAsnValCysAspSerGluAsnProGlySerGluGluProLysGlnGluLysGly
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SerVallleArgHisLeuGlnSerValThrGlySerLysIleArgValIleAspAspIle
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                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                       1.71e-10
265.00
38.66%
23.68%
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                                                                                                                      Similarity:
                                                                                                      Percent Similarity:
Best Local Similari
C;Genetics:
A;Gene: F19C24.19
A;Map position: 1
                                                          Alignment Scores:
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us-09-270-437d-7.rpr

à	371 GCGCCGAGGGGCTTTGGCTCTCGGGGTCAGCCCCGCCAGGGCTCACCTGTGGCAGGG	TGTGGCAGCGGG 430	
qq	297	 IleProGlnAsnLeuMe 302	
ζζ	431 GGCCCCAGCCAAGCAAGCAAGCAAGCAATCCCCCTTCGGCTCCTGGTGCCCAGTA	GCCCACCCAGTA 490	
Db	302	lGluGlyLysTy 321	
λŏ	491 TGTGGGTGCCATTATTGGCAAGGGGGCCACCATCGCGAACATCAAAACAGGCCACA	AAAACAGACCCA 550	
Db	321	aSerSerThrAr 341	
οy	551 GTCCAAGATAGACGTGCATAGGAAGAGAGAGAACGCAGGTGCAGCTGA	-GGTGCAGCTGA 595	
Db	341 gCysArgValAspPheValAsnLeuSerLysLysGluArgThrVal	uGlyAsnAsnAs 361	
λ δ,	596 AAAAGCCATCAGTGCACTCCACCCTGAGGCTGCTCCTCCGCTTGTAAGATGATCTT		
Q C			
δ fa	656 GGAGATTATGCATAAAGAGGCTAAGACCCAAAACGGCTGACGAGGTTCCCCT	CGAGGTTCCCCT 709 :::	
λŏ	710		
qq		 aGlySerSerIl 421	
Qy	770	812	
qa	: :::::: 421 elysGlulleMetGlnLysThrGlyThrAsnlleThrValThrLysTyrIleGluProPr	rileGluProPr 441	
ΟY	813	AGAGGACCATCAC 856	
DÞ	::: 441 oGlyGlyIleSerGlyLeuThrAla		
٥٧	857 TGTGAAGGGGGCCATCGAGAATTGTTGCAGGGCCGAGCAGGAATAATGAAGAAGT	PATGAAAAGT 913	
qa	461	eSerAlaLysLe 481	
ζ	914 TCGGGAGCCTATGAGAAATGTGTGCTGCCATGAGCTCTCACCTGATCCC	ATCCC 964	
Db	481	InCysProMetPr 501	
Qy	965 IGGCCTGACCTGCTGTAGGTCTTTTCCCAGCTTCATCCAGCGCAGTCCG	AGTCCCG 1019	
Db	501		
Οy	1020CGGCCTCCCAGCAGGGTTACTGGGGCTGCTCCCTAT	1055	
Db	521 oHisPhell	laSerSerGlnHi 541	
۸۵	1056AGCTCCTTTATGCAG	1070	
Db	541	euGlnIleGlnPr 561	
δλ	1071GCTCCCGAGCAGGAGATGGTGCAGGTGTTTATCCCCGCCCAGGCAGTGGCGCCAT	CAGTGGGCGCAT 1126	
QC	561	::: ::	
δ	1127	SCGCCTCCATCAA 1186	
Db	581 ulleGlyAlaLysGlyLysAsnIleLysMetIleIleArgAspThrGlyAlaSerValLy	lyAlaSerValLy 601	
δγ	1187 GATTGCACCCGAAACACCTGACTCCAAA	1217	
Db	601 sileGluAlaProGluGluLysThrGlnArgGluAlaGluGluAlaGluLysLysArgLy	luLysLysArgLy 621	
Qy	, 1217	1217	
Db	621 sLeuAspGluThrAspSerGlyCysGluGlyValAlaSerGlyAspHisProGlnGluPh	isProGlnGluPh 641	
δý	, 1217	1217	

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                               ----GITCGTATGGTTATCATCACCGCCAGAGGCCCAATTCAAGGCTCAGGGAAG 1273
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641 eLeuGluAspAsnAlaThrIleAsnSerSerAspAlaIleGluGluLysProLysProVa 661
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681 rValPheSerLysIleAlaGluThrSerSerSerLeuProSerSerGlyMetAspGlyAs
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pArgSerHisMetLeuArgIleArgThrGluValSerValProThrArgIleIleGlyAr
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741 llysileProGluGluArgAsnGlyGlyGluValTyrArgHisAspAspGlyLeuGl
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                                                                                             1274 AATCTATGGCAAACTCAAGGAGGAGAACTTCTTTGGTCCC-------
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830 yThrile----
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845 rValSer 847
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RESULT

p96554
hypothetical protein F19C24.19 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: D96554
R;Theologis, A: Bcker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Residues: 1-621 <STO>
A;Coss-references: GB:AE005173; NID:g11094762; PIDN:AAG29695.1; GSPDB:GN00141

Title: Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Minimum DB seq Maximum DB seq

Searched:

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A;Gene: CESP:MB8.5
A;Map position: 3
A;Introns: 38/3; 96/1; 133/3; 255/3; 307/3; 395/2; 436/2; 492/3; 657/3; 759/1; 820/1
                                                                                                                                                                                                                                                                            hypothetical prote
protein C08H9.2 [i
SCP160 protein - y
hypothetical prote
hypothetical prote
hypothetical prote
probable proline-r
F14M2.18 protein -
glutenin high mole
related to SCP160
                                                                                                                                                                                       transformation upr
single-stranded nu
kappa-B motif-bind
hnRNP complex prot
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hypothetical 24.7K
immediate-early pr
MHC class III hist
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eyelid - fruit fly
glutenin, high mol
MHC class III hist
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                                                                   hypothetical prote
vigilin - chicken
probable RNA-bindi
                                                                                                            rna binding protei
hnRNP protein E2 -
dC stretch-binding
                                                aypothetical prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cispecies: Caenorhabditis elegans
Cispecies: Caenorhabditis elegans
Cispecies: Caenorhabditis elegans
Cispecies: Caenorhabditis elegans
Cispecies: Caenorhabditis elegans
Cispecies: T3837
Silaton, J.
Submitted to the EMBL Data Library, June 1994
A;Reference number: Z19806
A;Reference number: Z19806
A;Reference number: Z19806
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-854 <MIL>
A;Residues: 1-854 <MIL>
A;Cross-references: EMBL:Z34802; PIDN:CAA84338.1; GSPDB:GN00021; CESP:M88.5
A;Experimental source: clone M88
Cigenetics: Association of the Caenorhabdition of the Caenorha
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-MODEL=frame+ n2p.model -DEV=xlp
-Q=/cgn2 1/USFTO spool p/US09270437/runat 23072004 095740 27439/app query.fasta_1.5582
-DE=FIR 78 -QFMT=fastan -SUFFIX=rspr -MINM_TCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LifsT=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-UOTFWH=pto -NORM=ext + HRAPSIZES=500 -MINIEN=0 -MAXIEN=200000000
-USER=US09270437 @CGN 1 1 134 @runat_23072004 095740_27439 -NCDU=6 -ICPU=3
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPENOCK=100 -LONGLOG
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -SPENEORE100 -LONGLOG
-PEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Matches:
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Mismatches:
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FILE REFERENCE: 210121.455C19
CURRENT PELLING NUMBER: US/10/313,986
CURRENT FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 560
SOFTWARE: EastSEQ for Windows Version 4.0
SEQ ID NO 348
LENGTH: 579
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ORGANISM: Homo
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APPLICANT: MONADA, Andria
APPLICANT: MATANADA, Andria
APPLICANT: Reed, Steven G.
APPLICANT: Reed, TONGTONG
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
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US-10-313-986-348
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Best Local Similarity:
Query Match:
DB:
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US-10-117-982-480
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Pred. No.:
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US-10-117-982-480
| Sequence 480, Application US/10117982
| Publication No. US20030138438A1
| GENERAL INFORMATION:
| APPLICANT: Foy, Teresa M. | APPLICANT: Vedvick, Thomas S. |
| APPLICANT: Carter, Darrick
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Conservative:
Mismatches:
Indels:
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                                                                                                                                 METHODS FOR
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Spies, Gregory A.
APPLICANT: Fan, Liqun
APPLICANT: Fan, Liqun
APPLICANT: Mang, Tongtong
APPLICANT: Mang, Tongtong
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CP
FILE REFERENCE: 21012.1455C18
CURRENT FILING DAIE: 2002-04-05
NUMBER OF SEQ ID NOS: 484
SOFTWARE: FASTSEQ for Windows Version 4.0
SENGTH: 579
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APPLICANT: Carter, Thomas S.

APPLICANT: Carter, Darrick
APPLICANT: Matanabe, Yoshihiro
APPLICANT: Henderson, Robert A.

APPLICANT: Henderson, Robert A.

APPLICANT: Matanabe, Yoshihiro
APPLICANT: Henderson, Robert A.

APPLICANT: Marcicle, Barbara
APPLICANT: Spies, Gregory A.

APPLICANT: Fan, Liqun
APPLICANT: Fan, Liqun
APPLICANT: Mang, Tongtong

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REPERBORE: 210121-455C18

CURRENT FILING DATE: 2002-04-05

NUMBER OF SEQ ID NOS: 484

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 579
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Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
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Sequence 449, Application US/10117982 Publication No. US20030138438A1 GENERAL INFORMATION:

APPLICANT: Foy, Teresa M.

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Best Local Similarity:
                                                                                                                                                                                                                  ; ORGANISM: Homo
US-10-117-982-446
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Pred. No.:
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GENERAL INCRMATION.
APPLICANT: Foy, Teresa M.
APPLICANT: Foy, Teresa M.
APPLICANT: Foy, Teresa M.
APPLICANT: Fanger, Gary R.
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Garter, Darrick
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Fan, Liqun
APPLICANT: Fan, Liqun
APPLICANT: Fan, Liqun
APPLICANT: Fan, Liqun
APPLICANT: Wang, Tongtong
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER
FILE REFERENCE: 210121.455C18
CURRENT APPLICATION NUMBER: US/10/117,982
CURRENT FILING DATE: 2002-04-05
NUMBER OF SEQ ID NOS: 484
SEQ ID NOS: 484
SEQ ID NO 446
SEQ ID NO 446
TENGTH: STP
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380
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                                                  APPLICANT: FOY, TETESA M.
APPLICANT: FOY, TETESA M.
APPLICANT: FOY, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Watenabe, Yoshihiro
APPLICANT: Matenabe, Yoshihiro
APPLICANT: Matenabe, Yoshihiro
APPLICANT: Matenabe, Michael D.
APPLICANT: Marios, Michael D.
APPLICANT: Marios, Michael D.
APPLICANT: Mariole, Barbara
APPLICANT: Fan, Liqun
APPLICANT: Fan, Liqun
APPLICANT: Wan, Tongtong
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TILLE OF INVENTION: ADD DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C18
CURRENT APPLICATION NUMBER: US/10/117,982
NUMBER OF SEQ ID NOS: 484
SOCTHARS: FASTSEQ FOR WINDOWS Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative:
Mismatches:
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Matches:
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        Sequence 348, Application US/10117982
Publication No. US20030138438A1
GENERAL INFORMATION:
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CRGANISM: Homo sapiens
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|AspileAlaSerMetAsnLeuGlnAlaHisLeuIleProGlyLeuAsnLeuAsnAlaLeu 373
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|SeralaalaCysLysSerIleLeuGluIleMetHisLysGluAlaGlnAspIleLysPhe
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             AAGGAAGGACGGAACCTGAAGAAGGTAGAGCAAGATACCGAGACAAAAATCACCATCTCC
<u> AAGGAGAACGCAGCTGCAGCTGAAAAAGCCATCAGTGTGCACTCCACCCCTGAGGGCTGC</u>
                                                              TCCTCCGCTTGTAAGATGATCTTGGAGATTATGCATAAAGAGGCGTAAGGACACCAAAACG
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GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Weng, Anjun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Li, Samual X.
APPLICANT: Li, Samual X.
APPLICANT: Henderson, Robert A.
APPLICANT: MCNeill, Patricia D.
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1875.00
84.68%
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Best Local Similarity:
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AspileAlaSerMetAsnLeuGlnAlaHisLeuIleProGlyLeuAsnLeuAsnAlaLeu 373
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LysGluAsnAlaGlyAlaAlaGluLysSerIleThrIleLeuSerThrProGluGlyThr
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US-10-007-700-449
; Sequence 449, Application US/10007700
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137 AsplysLeuAsnGlyPheGlnLeuGluAsnPheThrLeuLysValAlaTyrIleProAsp 156 GluThrAlaAlaGlnGlnAsnProLeuGlnGlnProArgGlyArgArgGlyLeuGlyGln 176 CTGGACAGCCTGCTCAGTATGGTACAGTAGAGAACTGTGAGCAAGTGAACACCGAG GAGCAGATAGCA----CAGGGACCTGAGAATGGGCGCCCGAGGG-----GGCTTTGGCTCT CysAspLeuProLeuArgLeuLeuValProThrGlnPheValGlyAlaIleIleGlyLys CGGGTTAGGAGCCGGAAATTCAAATCCGAAATATTCCACCCCAGCTCCGATGGGAAGTA AGTGAGACGCCAGTGAGTGTCACCTATTCCAACCGGGAGCAGACCAGGCAAGCCATC ATGAAGCTGAATGGCCACCAGTTGGAGAACCATGCCCTGAAGGTCTCCTACATCCCCGAT CGGGGTCAGCCCCGCCAGGGCTCACCTGTGGCAGCGGGGGCCCCCAGCCAAGCAGCAGCAA GTGGACATCCCCCTTCGGCTCCTGGTGCCCCACCCAGTATGTGGGGTGCCATTATTGGCAAG GAGGGGGCCACCATCCGCAACATCACAAAACAGACCCAGTCCAAGATAGACGTGCATAGG THE THERAPY 579 380 51 62 16 Length:
Matches:
Conservative:
Mismatches:
Indels: US-09-270-437D-7 (1-1946) x US-10-007-700-449 (1-579) OS FOR 1 APPLICANT: Wang, Aljun,
APPLICANT: Wang, Aljun,
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Rederson, Robert A.
APPLICANT: Panger, Neil
APPLICANT: Retter, Marc W.
APPLICANT: Penger, Neil
APPLICANT: Perfer, Marc W.
APPLICANT: Peckman, David W.
APPLICANT: Gatter, Darrick, Thomas S.
APPLICANT: Peckman, David W.
APPLICANT: Catter, Darrick
APPLICANT: Catter, Darrick
APPLICANT: Cot, Teresa M.
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                                                           APPLICANT: REMESSON, SOCIAL D. APPLICANT: REMESSON, SOCIAL D. APPLICANT: Renger, Neil APPLICANT: Renger, Neil APPLICANT: Renger, Neil APPLICANT: Panger, Marc W. APPLICANT: Fanger, Gary R. APPLICANT: Panger, Gary R. APPLICANT: Carter, Darrick APPLICANT: Carter, Darrick APPLICANT: Peckman, David W. APPLICANT: Peckman, David W. APPLICANT: Poy, Teresa W. TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.455C17
CURRENT FILENC DATE: 2001-11-30
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 446
LENGTH: 579
                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
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           Skeiky, Yasir A.W.
Li, Samual X.
Kalos, Michael D.
Henderson, Robert A.
McNaill, Patricia D.
Fanger, Neil
Retter, Marc W.
Durham, Margarita
Fanger, Gary R.
Vedvick, Thomas S.
Carter, Darrick
Watanabe, Yoshihiro
Peckman, David W.
Cai, Feng
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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; Publication No. US20030064947A1
; GENERAL INPORMATION:
; APPLICANT: Wang, Tongtong
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Kalos, Michael D.
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McNeill, Patricia
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354 AspIleAlaSerMetAsnLeuGlnAlaHisLeuIleProGlyLeuAsnLeuAsnAlaLeu 373
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APPLICANT: Wang, Tongtong APPLICANT: Wang, Aljun APPLICANT: Skeiky, Yasir A.W. APPLICANT: I, Sammal X.
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APPLICANT: MONeill, Patricia D.
APPLICANT: Fanger, Neil
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Gary R.
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APPLICANT: Vedvick, Thomas S.
APPLICANT: Watanabe, Yoshihiro
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APPLICANT: Cai, Feng M.
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APPLICANT: Cai, Feng M.
APPLICANT: Compositions and Merhods FOR THE FILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.455C17
CURRENT APPLICATION NUMBER: US/10/007,700
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 348
LENGTH: 579
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APPLICANT: Marnerakis, Margarita
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APPLICANT: Fanger, Gary
APPLICANT: Carter, Darrick
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APPLICANT: Watanabe, Yoshihiro
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                     GAGAATTGTTGCAGGCCCGAGCAGGAAATAATGAAGAAAGTTCGGGAGGCCTATGAGAAT
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Sequence 449, Application US/09897778 Patent No. US20020147143A1

US-09-897-778-449; Sequence 449, Ar.; Patent No. US200

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GluGlyAlaThrIleArgAsnIleThrLysGlnThrGlnSerLysIleAspValHisArg
                        AAGGAGAACGCAGGTGCAGCTGAAAAAGCCATCAGTGTGCACTCCACCCCTGAGGGCTGC
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452 161 221 116 281 136 341 156 392 176 193 213 572 233 632 253 96 102 CGGGTTAGGAGCCGGAAAATTCAAATCCGAAATATTCCACCCCAGCTCCGATGGGAAGTA CTGGACAGCCTGCTGGCTCAGTATGGTACAGTAGAAACTGTGAGCAAGTGAACACCGAG 282 ATGAAGCTGAATGGCCACCAGTTGGAGAACCATGCCCTGAAGGTCTCCTACATCCCCGAT GGCTTTGGCTCT 157 GluThralahlaGlnGlnAsnProLeuGlnGlnProArgGlyArgArgGlyLeuGlyGln CGGGGTCAGCCCCGCCAGGGCTCACCTGTGGCAGCGGGGCCCCCAGCCAAGCAGCAGCAA 513 GAGGGGCCACCATCCGCAACATCACAAAACAGACCCAGTCCAAGATAGACGTGCATAGG AAGGAGAACGCAGGTGCAGCTGAAAAAGCCATCAGTGTGCACTCCACCCCTGAGGGCTGC GTGGACATCCCCCTTCGGCTCCTGGTGCCCACCCAGTATGTGGGGTGCCATTATTGGCAAG THE THERAPY 579 380 51 62 16 GAGCAGATAGCA---CAGGGACCTGAGAATGGGCGCCGAGGG Sequence 446, Application US/09897778
Fatent No. US20020147143A1
GENERAL INNORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Marnerakis, Margarita
APPLICANT: Panger, Gary R.
APPLICANT: Panger, Gary R.
APPLICANT: Peckham, Darick
APPLICANT: Peckham, David W.
APPLICANT: Henderson, Robert A.
APPLICANT: Peckham, David W.
APPLICANT: Peckham, David W.
APPLICANT: Peckham, David W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER;
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER;
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER;
TITLE FERENCE: 21011455C16
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FASESED for Windows Version 4.0
SEQ ID NO 446
LENGTH: 579 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: US-09-270-437D-7 (1-1946) x US-09-897-778-446 (1-579) 1.52e-133 1875.00 84.68* 74.66* 53.10*

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GAGCAGATAGCA---CAGGGACCTGAGAATGGGCCCCGAGGG-----GGCTTTGGCTCT 392
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                                                                                                                                                            US-UG-8977/8 Application US/0989778
Patent No. US20020147143A1
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Marnerakis, Margarita
APPLICANT: Fanger, Gary R.
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Pecklam, Nobert A.
APPLICANT: Pecklam, Nobert A.
APPLICANT: Pecklam, Nobert A.
APPLICANT: Pecklam, Nobert A.
APPLICANT: Pecklam, Nobert A.
APPLICANT: Penger, Neil
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-348
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Best Local Similarity:
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| AspileAlaSerMetAsnLeuGlnAlaHisLeuIleProGlyLeuAsnLeuAsnAlaLeu 373
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        CysAspLeuProLeuArgLeuLeuValProThrGlnPheValGlyAla11e11eGlyLys
                                                                                             GluGlyAlaThrIleArgAsnIleThrLysGlnThrGlnSerLys1leAspValHisArg
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Fatent No. USA020110N1
FAPLICANT: Reter, Marc W.
FILLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C15
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARER FEASTSQ for Windows Version 3.0
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APPLICANT: Fan, Liqun
APPLICANT: Ralos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Ranger, Neil
APPLICANT: Fanger, Neil
ITILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
ITILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REPERENCE: 210121.455C14
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTWARE: Faster Falson
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APPLICANT: Watanabe, Yoshihiro
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APPLICANT: Wang, Tongtong
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-DB=Published Applications AA -QFWT=fasta_1 - SUFFIX=reapb - MINMATCH=0.1
-LOOPEXT=0 -LOOPEXT=0 -UNITS=blts -START=1 - RND=-1 - MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 - DOCALIGN=200 - THR SCORE-petc - THR_MAX=100
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-LONGLOG - DEV TIMEOUT=20 - WARN TIMEOUT=30 - THREADS=1 - XGAPEXT=0.5
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1. /cgn2_6/ptodata/2/pubpaa/USO7_puBCOMB.pep:*

2. /cgn2_6/ptodata/2/pubpaa/PCT_MEM_PUB_pep:*

3. /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

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699GAGGITCCCCTGAAGATCCTGGCCCATAATAACTTTGTAGGGCGTCTCATTGGCAAG 755 184 GlyAsnAlaValGlnGluIleMetIleProAlaSerLysAlaGlyLeuVallleGlyLys	756 GAAGGACGGAACCTGAAGAAGGTAGAGATACCGAGACAAAAATCACCATCTCCTCG 815	816 TIGCAAGACCITACCCITTACAACCCIGAGAGGACCAICACIGIG 860 :::	AAGGGGCCATCGAGAATT ThrelwaenDrotwrwev	 258 GlnGlyGlyPheArgGluValArgAsnGluTyrGly269	966 GGCCTGAACCTGGCTGTTGTGTTTTCCCAGCTTCATCCAGCGCAGTCCCGCCT 1025	CCCAGCAGCGTTACTGGGGCTGCTCCTTATAGCTCCTTTATGCAGGCTCCCGAGCAGGAG	::: 270SerArg11eG1yG1y	1086 ATGGTGCAGGTGTTTATCCCCGCCCAGGCAGTGGCGCCATCATCGGCAAGAAGGGGCAG 1145	CACATCAAACAGCTCTCCCGGTTTGCCAGCGCCTCCATCAAGATTGCACCACCGGA	:::::: 297 MetlleLysLysIleGlnAsnAspAlaGlyValArgileGlnPheLysProAspAspGly 316	1203ACACCIGACICCAAAGTICGIAIGGITAICAIGAACGCCAGAGGCCCAA 1256	317 ThrThrProGluArgileAlaGlnileThrGlyProProAspArgCysGln 333	1257 TTCAAGGCTCAG1268	334 HisAlaAlaGlullelleThrAspLeuLeuArgSerValGlnAlaGlyAsnProGlyGly 353	1269GGAAGAATCTATGGCAAACTCAAGAGAGAGAACTTCTTTGGTCCCAAG 1316	354 ProGlyProGlyĠlyArgGlyArgGlyArgGlyGlnGlyAsnTrpAsnMetGlyProPro 373	1317 GAGGAAGTGAAGCCGACATACGTGTGCCAGCATCAGCAGCTGGCGGGTCATT 1376	392	1377 GGCAAAGGTGGAAAAAGGTGAACGAGTTGCAGAATTTGACGGCAGCTGAGGTGGTAGTA 1436 	1437 CCAAGAGACCAGACCCCTGATGAGAACGACCAGGTCATCGTGAAAATCATCGGACAT 1493	::: :::	1494TTCTATGCCAGTCAGATGGCTCAACGGAAGATCCGAGACAT 1534	433 ProGlnGlnIleAspTyrAlaArgGlnLeuIleGluGluLysIleGlyGlyBroValAsn 452	1535 CCTGGCCCAGGTTAAGCAGCAGCATCAGAAGGGACAGAGTAACCAGGCCCAGGCACG 1591	453 ProLeuglyProProValProHisGlyProHisGlyValProGlyProHisG 470	1592 GAGGAAGTGACCAGCCCTTGCCTGTCCCTTNGA 1624	
Qy 699 Db 184	Qy 75	Qy 81.		Db 25	Qy 96			Oy 108			Qy 120:	Db 31	Qy 125	Db 33		35 qa			Qy 137 Db 39	Qy 143	Db 41	Qy 149	Db 43	Qy 153	Db 45	Qy 159	40

1625 GTCCAGGA	633	1670 CAGGCCTGAGAATGAGTGGGAATCCGGGACACNTGGGCCGGGCTGTAGATGAGGTTTGCC 1729 	1730 CACTIGATIGAGAAAAGAIGTICCAGIGAGGAACCCTGAICINTCAGCCCGAACACCCAC 1789 :::::: 543 HisTyrTyrGlnGlnAlaGlnProProProFroAlaAla 555	1790 CCAATTGGGCCAACACTGINTGCCCCTCGGGGTGTCAGAAAITNTAGCGCAAGGCAC 1846 	1847 TTTTAAACGIGGATIGTTIAAAGAAGCICTCCCAGGCCCCACCAAGAGGGGGATCACACC 1906 :::	907
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IDBNITEICATION METHOD:
OTHER INFORMATION: Amino Acid 149 (Xaa)
NAME: WILLIAM S. FEILER
REGISTRATION NUMBER: 26,728
REFERENCE/DOCKET NUMBER: 2026-4063PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEPHONE: (212) 751-6849
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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22.39%
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Best Local Similarity:
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CELL LINE: FORGANELLE:
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                                                        -----TTCTATGCCAGTCAGATGGCTCAACGGAAGAT-----CCGAGACAT 1534
                                                                                                                                   CCT---GGCCCAGGTTAAGCAGCAGCATCAGAAGGGACAGAGTAACCAGGCCCAGGCACG 1591
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                                                                                    470 lyProProGlyProProGlyProGlyThrProMetGlyProTyrAsnProAlaProTyrA 490
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490 snProGlyProProGlyProAlaProHisGlyProProAlaProTyrAlaProGlnGlyT 510
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   --TCAGTGGGAAGAAAATAAAATTTCCTTCAGGT 1939
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APPLICANT: AS REPRESENTED BY THE SECRETARY, DEPARTMENT OF
APPLICANT: HEALTH AND HUMAN SERVICES
TITLE OF INVENTION: NOVEL FUSE BINDING
TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProAlaGlyAlaProThrThrThrGlnThrAsnGlyGlnGlyAsp----
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                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/021,608
FILING DATE: 22-FEB-1993
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: FLOPPY DISK COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-
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CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN &
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
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                                                                                                                                             GCTGAAAAAGCCATCAGTGTGCACTCCACCCTGAGGGCTGCTCCTCCGCTTGTAAGATG
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| ProGluArgSerCys***LeuThrGlyThrProGluSerValGlnSerAlaLysArgLeu
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222 IledinAsp------GlyProGinAsnThrGlyAlaAspLysProLeuArgIle
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297 MetileLysLysIleGlnAsnAspAlaGlyValArgIleGlnPheLysProAspAspGly
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317 ThrThrProGlu-----ArgileAlaGlnIleThrGly&roProAspArgCysGln
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164 LeuAspGlnIleValGluLySGlyArgProAlaProGlyPheHisHisGlyAspGlyPro
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                                                                      258 GlnGlyGlyPheArgGluValArgAshGluTyrGly-
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Matches:
Conservative:
Mismatches:
Indels:
   APPLICANT: ROBERT C., AND AVIGAN, MARK I.
ITILE OF INVENTION: NOVEL FUSE BINDING
ITILE OF INVENTION: PROTEIN AND CDNA THEREFOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM S. FEILER
REGISTRATION NUMBER: 26,728
REFERENCE/DOCKET NUMBER: 2026-4063US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                     MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION UNDERS: US/08/726,160
FILING DATE: 04-0CT-1996
CLASSIFICATION NATA:
APPLICATION NATA:
RAPLICATION NATA:
APPLICATION NATA:
APPLICATION NATA:
APPLICATION NATA:
APPLICATION NAMBER: 08/021,608
FILING DATE: 22-FEB-1993
CLASSIFICATION: 435
                                                                                           ADDRESSEE: MORGAN & FINNEGAN STREET: 345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide/Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114 TCACCTGTGGCAGCGGG-
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36.46%
22.39%
6.94%
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STRANDENESS: Single
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide/P
HYPOTHETICAL: No
                                                                                                                                                                                       ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY I
                                                                              CORRESPONDENCE ADDRESS:
                                                         NUMBER OF SEQUENCES:
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OTHER INFORMATION:
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CELL LINE: HL60
                                                                                                                               CITY: NEW YORK STATE: NEW YORK COUNTRY: USA
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Pred. No.:
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rcent Similarity: 36.46% Conservative: 93 st Local Similarity: 22.39% Mismatches: 219 ery Match: 1.94% Indels: 202 -09-270-437D-7 (1-1946) x US-08-021-608D-2 (1-644) 309 AACCATGCCTGAAGGTCTCCTACATCCCCGATGAGCAGATAGCACAGGGACCT	Db 28 AsnAspAlaPheLysAspAlaLeuGlnArgAlaArgGlnIleAlaAlaLysIleGlyGly 47 Qy 363 GAGAATGGGCGCCGAGGGGTTTGGTTCTCGGGGTCAGCCCCGCAGGGC 413 :::	432GCCCCAGCCAAGCAGCAAGTGGACATCCCCCTTCGG	Db 125 ArgileGinGinGiuSerGlyCysLysIleGinIleAlaProAspSerGlyGlyLeu 143 Qy 591 GCTGAAAAAGCCATCAGTGCACTCCACCCCTGAGGGCTGCTCCTGCGCTTGTAAGATG 650 [699GAGGTTCCCCTGAAGATCCTGGCCCATAATAACTTTGAGGGGGTCTCATTGGAAGA 1::	Qy 816 TTGCAAGACCTTACCACTTACAACCCTGAGAGGACC	Db 258 GlnGlyGlyPheargGluValargAsnGluTyrGly

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21 LysValGluGlnAspThrGluThrLysIleThrIleSerSerLeuGlnAspTeuThrLeu 40
                                                                                                                     774 AAGGTAGAGCAAGATACCGAGACAAAATCACCATCTCCTCGTTGCAAGACCTTACCCTT
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; Patent No. 5580760
; GENERAL INFORMATION:
   APPLICANT: LEVENS, DAVID L., DUNCAN,
   ATILE OF INVENTION: NOVEL FUSE BINDING
   TITLE OF INVENTION: PROTEIN AND CONA THEREFOR
   NUMBER OF SEQUENCES: 24
   CORRESPONDENCE ADDRESS:
   ADDRESSEE: MARGAN & FINNEGAN
                                                                                US-09-270-437D-7 (1-1946) x US-09-261-855-18 (1-49)
    Mismatches:
Indels:
                                                                                                                                                                                                                                                                               834 TACAACCCTGAGAGGACCATCACTGTG 860
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22-FEB-1993
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NAME: WILLIAM S. FETLER
REGISTRATION NUMBER: 2026
TELECOWNUTICATION INFORMATION:
TELECOWNUTICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEPAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 644
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  100.00%
6.94%
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APPLICATION NUMBER: US
FILING DATE: 22-FEB-19
CLASSIFICATION: 435
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STRANDEDNESS: Single
TOPOLOGY: Unknown
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MEDIUM TYPE: FLOPPY
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CLASSIFICATION: 435
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NEW YORK
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FEATURE:
Best Local Similarity:
Query Match:
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Pred. No.:
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                                             1419 GCAGCTGAGGTGGTAGTACCAAGAGACCAGACCCCTGATGAGAACGACCAGGTC---ATC 1475
                                                                                                                                                                                                     1524 AT-----CCGAGACATCCT---GGCCCAGGTTAAGCAGCATCAGAAGGGACAGAG 1573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1712 CTGTAGATCAGGTTTGCCCACTTGATTGAGAAAGATGTTCCAGTGAGGAACCCTGATCTN 1771
                                                                                                                         -- TICTATGCCAGTCAGATGGCTCAACGGAAG 1523
                                                                                                                                                                                                                                                                                                                                                                                                                                             CAACAACGGGCAGAAATCG 1651
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                                                                                                                                             426 PheThrileArgGlyThrProGlnGlnIleAspTyrAlaArgGlnLeuIleGluGluLys 445
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-----GlnGlnAsnProAlaProAla 576
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      386 LysThrGlyLeullelleGlyLysGlyGlyGluThrileLysSerileSerGlnGlnSer 405
                                                                     406 GlyAlaArgIleGluLeuGlnArgAsnProProProAsnAlaAspProAsnMetLysLeu 425
                                                                                                                                                                                                                              523 sp-------ProAlaLysAlaGlyThrAspProAsnSerAla-AlaTrpAlaAla 538
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US-09-261-855-18
Squence 18, Application US/09261855A
Squence 18, Application US/09261855A
Patent No. 6255055
GENERAL INFORMATION:
TITLE OF INVENTION: TREE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
CURRENT PELLICATION NUMBER: US/09/261,855A
CURRENT FILING DATE: 199-03-03
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PATENTIN Ver. 2.0
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                                                                                                                                                                                                                                                                                   GGAAGTGACCAGCCCTC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              539 Tyr-----TyrAlaHisTyrTyrGlnGlnAla------
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Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                 1612 ----CCTGTCCCTTNGAGTCCAGGA---
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                                                                                                                         1476 GTGAAAATCATCGGACAT--
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245.00
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597 ProAlaProThrGly 601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              948 AGCTCTCACCTGATCCCTGGCCTGAACCTGGCTGTTGGGTCTTTTCCCAGCTTCATCC 1007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1008 AGCGCAGTCCCGCCGCCTCCCAGCATTACTGGGGCTGCTCCCTATAGTCTTTATG 1067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1068 CAGGCTCCCGAGCAGGAGATGGTGCAGGTGTTTATCCCCGGCCCAGGCAGTGGGCGCCATC 1127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 310 PheLysProAspAspGlyThrThrProGlu-----ArglleAlaGln1leThrGly 326
                                                                                              SerValMetThrGluGluTyrLysValProAspGlyMetValGlyPheileileGlyArg 117
                                                                                                                                  572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    327 ProProAspArgCysGlnHisAlaAlaGluIleIleThrAspLeuLeuArgSerValGln 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         347 AlaGlyAsnProGlyGlyProGlyGlyArgGlyArgGlyArgGlyGlnGlyAsn 366
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|TrpAsnMetGlyProProGlyGlyLeuGln---GluPheAsnPheIleValProThrGly 385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---GlyProGlnAsnThrGlyAla
                       -GlnGlnGlnArg
                                                           453 GTGGACATCCCCCTTCGGCTCCTGGTGCCCACCCAGTATGTGGGTGCCATTATTGGCAAG
                                                                                                                                  513 GAGGGGCCACCATCCGCAACATCACAAAACAGACCCAGTCCAAGATAGACGTGCATAGG
                                                                                                                                                                                                           573 AAGGAGAACGCAGGTGCAGCTGAAAAAGCCATCAGTGTGCACTCCACCCCTGAGGGCTGC
                                                                                                                                                                                                                                633 TCCTCCGCTTGTAAGATGATCTTGGAGATTATGCATAAA-----GAGGCTAAGGACACC
                                                                                                                                                                                                                                                                                                         ---GAGGTTCCCCTGAAGATCCTGGCCCATAATAACTTTGTA
                                                                                                                                                                                                                                                                                                                                                                                          177 HisHisGlyAspGlyProGlyAsnAlaValGlnGluIleMetIleProAlaSerLysAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              852 ------ATCACTGTGAAGGGGCCATCGAGAATTGTTGCAGGCCGAGCAGGAAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -GCCTATGAGAATGATGTGGCTGCCATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          251 LeuGluLeuIleArgAspGlnGlyGlyPheArgGluValArgAsnGluTyrGly----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------AsnGluGlyIleAspValProileProArgPheAlaValGlyIleVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       798 AAAATCACCATCTCCTCGTTGCAAGACCTTACCCTTTACAACCCTGAGAGGACC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      269 ------SerArgileGlyGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .242 CCGCCAGAG---GCCCAATTCAAGGCTCAG----
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217 LysMetValMet-----IleGlnAsp-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       903 ATGAAGAAAGTTCGGGAG----
             :::
88 GlnLeuProProMetHis-
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APPLICANT: THE GOVERNMENT OF THE UNITED STATES
APPLICANT: AS REPRESENTED BY THE SECRETARY, DEPARTMENT OF
APPLICANT: HEALTH AND HUMAN SERVICES
TITLE OF INVENTION: NOVEL FUSE BINDING
TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or Ile
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1140
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202
1189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 ProAspAlaLysLysValAla-----ProGlnAsn----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-270-437D-7 (1-1946) x PCT-US94-01782-10 (1-643)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/021,608
FILING DATE: 22-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM S. FEILER
REGISTRATION NUMBER: 26,728
REFERENCE/DOCKET NUMBER: 26,728
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels:
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                                                                                                                                                                                                                                                                                                                                                 UMBER: PCT/US94/01782
22-FEB-1994
                                                                                                                                                                                                                                                                                      SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
FILING name
                                                                                                                              ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: Peptide/Protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                   MEDIUM TYPE: FLOPPY DISK COMPUTER: IBM PC COMPATIBLE ODERATING SYSTEM: PC-DOS/MC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.81e-14
248.50
37.80%
22.33%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Single
                                                                                                                                                                                                                      ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL INPE:
ORGANELLE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: Sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCT-US94-01782-10
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                                                                                                                                                                                                       COUNTRY:
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US-08-726-160-10		4	210 DhalwaDroaenAenGlvTh
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Alignment Scores: Pred. No.: 8.81	Length:	ð	1242 CCGCCAGAGGCCCAATT
ty:	Conservative:	qu	327 ProProAspArgCysGlnHi
	22.33* Minmarches: 202 7.04\$ Indels: 189 1 Gabs: 32	à	
09-270-437D-7 (1-1946)	3-726-1	a	
OV 336 CCCGATGAGCE	-GAGCAGATAGCACAGGGACCTGAGAATGGGCGCCGAGGGGGTTTGGCTCT 392	ò	1299 AACTTCTTTGGTCCCAAGGA
73 ProAspAl	::: YThr	qa	
	<u> </u>	ζ	1359 GCAGCTGGCCGGGTCATTGG
		đ	386 LysThrdlyLeuileil
100 CHO CT.		ò	1419 GCAGCTGAGGTGGTAGTACC
Qy 453 GIGGACAICCCCC ::: Db 98 SerValMetThrGl		qq	
513 GAGGGG	TCCGCAACATCACAAAACAGACCCAGTCCAAGATAGACGTGCATAGG 572	à	
118	GlyGlyGluGlnIleSerArg1leGlnGlnGluSerGlyCysLysIleGlnIleAla 136	අි	PheThrile
573	AAGGAGAAAACGCAGGTGCAGCTGAAAAAGCCATCAGTGCACTCCACCCCTGAGGGCTGC 632	À	1524 ATCCGAGACATCC
137	::::::	අු .	
Qy 633 TCCTCCGCTTGTAA	TCCTCCGCTTGTAAGATGATCTTGGAGATTATGCATAAAGAGGCTAAGGACACC 686	ð í	TAACCAGGCCCA
:: Db 157 GlnSerAlaLysA:	:::::::: :::: :::: alysArgLeuLeuAspGlnIleValGluLysGlyArgProAlaProGlyPhe 176	a 6	OTAVIDOIA
Qy 687 AAAACGGCTGAC	GAGGTTCCCCTGAAGATCCTGGCCCATAATAACTTTGTA 737	Š	1812CIGICCCIINGGO ::: 183 vr&snPro&]aProTvr&sn
Db 177 HisHisGlyAspGl	177 HisHisGlyAspGlyProGlyAsnAlaValGluGlulleMetIleProAlaSerLysAla 196	8 8	
Qy 738 GGGCGTCTCATTGC	GGGCGTCTCATTGGCAAGGAAGGAACCTGAAGAAGGTAGAGCAAGATACCGAGACA 797	Z 60	503 roTyrAlaProGlnGlyTrp
Db 197 GlyLeuValileG	197 GlyLeuVallleGlyLysGlyGlyGlyThrileLysGlnLeuGlnGluArgAlaGlyVal 216	8	
Oy 798 AAAATCACCATCTC	798 AAAATCACCTCCTCGTTGCAAGACCTTACCTTTACAACCCTGAGAGGACC 851	7 A	
Db 217 LysMetValMet-	IleglnAspGlyProglnAsnThrGlyAla 230	} &	CTGTAGATCAGGI
Qy 852ATCA(ATCACTGTGAAGGGGCCATCGAGAATTGTTGCAGGGCCGAGCAGGAAATA 902	7 A	
Db 231 AspLysProLeuA	AspLysProLeuArglleThrGlyAspProTyrLysValGlnGlnAlaLysGluMetVal 250	}	TCAGCCCCCAAA
Qy 903 ATGAAGAAAGTTCGGGAG	GGGAG	i 2	
Db 251 LeuGluLeuIleAn	LeuGluLeuIleArgAspGlnGlyGlyPheArgGluValArgAsnGluTyrGly 268	l &	
Qy 948 AGCTCTCACCTGA:	AGCTCTCACCTGATCCCTGGCCTGAACCTGGCTGTAGGTCTTTTCCCAGCTTCATCC 1007	7 fd	
Db 268	268	}	
Qy 1008 AGCGCAGTCCCGC	AGCGCAGTCCCGCCGCCTCCCAGCAGCGTTACTGGGCTGCTCCCTATAGCTCCTTTATG 1067	3 6	577 GlvGlnValAspTvrThrLv
Db 269	SerArgileGlyGly	ò	
Qy 1068 CAGGCTCCCGAGC	11	g 6	::: 597 ProAlaProThrGly
Db 274A	78	RESULT	LT 11
1128	ATGGGCAAGAAGGGGCAGCACATCAAACAGCTCTCCCGGTTTGCCAGCGCCTCCATCAAG 1187	PCT-1	PCT-US94-01782-10; Sequence 10, Application PC/TUS9; Centers 11, Application PC/TUS9;
DD Z9U ileGiyArgAsnG		5 	EMERGIA INI CIRCUITORI

------GGAAGAATCTATGGCAAACTCAAGGAGGAG 1298 BAGGAAGTGAAGCTGGAGACCCACATACGTGTGCCAGCATCA 1358 GGCAAAGGIGGAAAAACGGIGAACGAGTIGCAGAATTIGACG 1418 CCAAGAGACCAGACCCCTGATGAGAACGACCAGGTC---ATC 1475 -----TTCTATGCCAGTCAGATGGCTCAACGGAAG 1523 CT---GGCCCAGGTTAAGCAGCAGCATCAGAAGGGACAGAG 1573 3A----- 1611 PAGGCCTGAGAATGAGTGGGAATCCGGGACACNTGGGCCGGG 1711 RCTTGATTGAGAAGATGTTCCAGTGAGGAACCCTGATCTN 1771 CAATTGGC---CCAACACTGTNTGCCCCTCGGGGTGTCAGA 1828 ITTIAAACGIGGAITGITIAAAGAAGCICICCAGGCCCCACC 1888 --ACACCTGACTCCAAAGTTCGTATGGTTATCATCACTGGA 1241 3TCCAGGA----- 1632 -----CAACAACGGCAGAAATCG 1651 -----TCAGTGGGAAAAATA 1924 |||::: |isAlaAlaGluIleIleThrAspLeuLeuArgSerValGln 346 roglyProglydrgGlyArgGlyArgGlyArgGlyAsn 366 ||||||||||||||:::||||::: 3]yLysGlyGlyGluThrIleLysSerIleSerGlnGlnSer 405 ProGlnGlnIleAspTyrAlaArgGlnLeuIleGluGluLys 445 ||| |||||| ProLeuGlyProProValProHisGlyProHisGlyVal--- 464 ::|||||| snProGlyProProGlyProAlaProHisGlyProProAlaP 503 rpGlyAsnAlaTyrProHisTrpGlnGlnGlnAlaProProA 523 :::|||::: ::: LysAlaTrpGluGluTyrTyrLysLysMetGlyGlnAlaVal 596 ||| isTyrTyrGlnGlnAla------FTCAAGGCTCAG-----59401782

OY 1652 ACAGTGTCCTCCCGGCAGGCCTGAGAATGAGTCCGGCACCACNTGCGCCCGGGT 1711	RESULT 10 US-00-726-160-10 IS-00-726-160-10 IS-00-726-160-10 IS-00-726-160-10 IS-00-726-160-10 IS-00-726-160-10 IS-00-726-160-10 IS-00-726-160-10 IS-00-726-10 IS	OD GOSH R 10 HASS CO
Qy 798 AAAATCACCATCCTCGTTGCAAGACCTTACCACTGAGAGGACC		Steur Steur GAAG HIYS AGAG ACAG ALAP ALAP ATCG ATCG

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137 ProAspSerGlyGlyLeuProGluArgSerCys***LeuThrGlyThrProGluSerVal 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    738 GGGCGTCTCATTGGCAAGGAAGGACGGAACCTGAAGAAGGTAGAGCAAGATACCGAGACA 797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          336 CCCGAT---GAGCAGATAGCACAGGGACCTGAGAATGGGCCCCGAGGGGCTTTGGCTCT 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             393 CGGGGTCAGCCCCGCCAGGGCTCACCTGTGGCAGCGGGGGCCCCCAGCCAAGCAGCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            453 GIGGACAICCCCCTICGGCICCTGGIGCCCCAGIAIGIGGGIGCCAITAITGGCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98 SerValMetThrGluGluTyrLysValProAspGlyMetValGlyPheileIleGlyArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         513 GAGGGGCCACCATCCGCAACATCACAAAACAGACCCAGTCCAAGATAGACGTGCATAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               573 AAGGAGAACGCAGGTGCAGCTGAAAAAGCCATCAGTGTGCACTCCACCCCTGAGGGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        687 AAAACGGCTGAC-----GAGGTTCCCCTGAAGATCCTGGCCCATAATAACTTTGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           633 TCCTCCGCTTGTAAGATGATCTTGGAGATTATGCATAAA-----GAGGCTAAGGACACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Amino Acid 148 (Xaa) is Met or Ile US-08-021-608D-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             643
140
97
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189
32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-270-437D-7 (1-1946) x US-08-021-608D-10 (1-643)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels:
                    UMBER: US/08/021,608D
22-FEB-1993
                                                                                                                                                                                                2026-4063
                                            FILING DATE: 22-FEB-1993
CLASSIFICATION: 435
PRIOR APPLICATION ATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM S. FEILER
REGISTRATION NUMBER: 26,728
REGISTRATION NUMBER: 2026
TELEPHONE: (212) 758-4800
TELEPAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 643
                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: Unknown MOLECULE TYPE: Peptide/Protein HYPOTHETICAL: No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88 GlnLeuProProMetHis--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.81e-14
248.50
37.80%
22.33%
WORDPERFECT 5.1
                 CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                Single
                                                                                                                                                                                                                                                                                                                 Amino Acid
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Best Local Similarity:
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                                                                     GATGTGGCTGCCATGAGC----TCTCACCTGATCCCTGGCCTGAACCTGGCTGTA
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US-08-021-608D-10

US-08-021-608D-10

Sequence 10, Application US/08021608D

GENERAL INFORMATION:

APPLICANT: LEVENS, DAVID L., DUNCAN,

APPLICANT: ROBERT C., AND AVIGAN, MARK I.

TITLE OF INVENTION: NOVEL FUSE BINDING

TITLE OF INVENTION: PROFIEIN AND CONA THEREPOR

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:
                                                                                                                                      GGTCTTTTCCCAGCTTCATCCAGCGCAGTCCCGCCG-
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MEDIUM TYPE: FLOPPY DISK
COMPUTER: IEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: NEW YORK
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Matches:
Conservative:
Mismatches:
Indels:
                             US/09/606,421B
FILE REFERENCE: 210121.455cy
CURRENT APPLICATION NUMBER: US/09/606,421;
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.(
SEQ ID NO 176
LENGTH: 579
LYPE: PRT
CRGANISM: Homo sapiens
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84.48%
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Best Local Similarity:
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                                          314 ProLeuGlnGluLeuThrLeuTyrAsnProGluArgThrlleThrValLysGlyAsnVal 333
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Sequence 176.4 Application US/09606421B

Sequence 176.4 Application US/09606421B

Sequence 176.4 Application US/09606421B

SEMERAL INFORMATION:
APPLICANT: Wang, Tongtong

APPLICANT: Ranger, Cary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Mancy
APPLICANT: Mancy Applicant: Applicant Applicant
APPLICANT: Wang, Aight
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Mancy Aight
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TYPE: PRT ORGANISM: Homo US-09-542-615A-176
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Sequence 176, Application US/09542615A
Patent No. 6518256
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.

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APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy A.
TITLEON: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CAN TITLE OF INVENTION: 210121.455C8
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SEQ ID NO 176
SEQ ID NO 176
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Sequence 176, Application US/09480884A
; Batent No. 6482597
; GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Fan, Liqun
; APPLICANT: Fan, Liqun
; APPLICANT: Fan, Canger, Michael D.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY;
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER;
FILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER;
FILE REPERENCE: 210121.455c6
; CURRENT APPLICATION NUMBER: US/09/480,884A
; NUMBER OF SEQ ID NOS: 330
; SOFTWARR: FastSEQ for Windows Version 3.0
; SEQ ID NO 176
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Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo
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GAGCAGATAGCA---CAGGGACCTGAGAATGGGCGCCGAGGG-----GGCTTTGGCTCT 392
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                APPLICANT: Wang, Tongtong
APPLICANT: Ran, Liqun
APPLICANT: Ran, Liqun
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CAN
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CAN
FILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSEQ for Windows Version 3.0
                       579
         1572 AGTAACCAGGCCCAGGCACGGAAG
                                                                          Sequence 176, Application US/09643597
Patent No. 6426072
GENERAL INFORMATION:
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US-09-643-597-176
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                                                                                  ThrGluGluIleProLeuLysIleLeuAlaHisAsnAsnPheValGlyArgLeuIleGly
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                  GAGGGGGCCACCATCCGCAACATCACAAAACAGACCCAGGTCCAAGATAGACGTGCATAGG
                                AAGGAGAACGCAGCTGAAAAAGCCATCAGTGTGCACTCCACCCCTGAGGGCTGC
                                                                                                                        TCCTCCGCTTGTAAGATGATCTTGGAGATTATGCATAAAGAGGCTAAAGACACAAAACG
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Oy 1518 CGGAAGATCCCAGACATCCTGGCCCAGGTTAAGCAGCAGCATCAGAAGGGACAG 1571 Db 551 ArglyslleGlnGlulleLeuThrGlnValLysGlnHisGlnGlnLysAlaLeuGln 570 Qy 1572 AGTAACCAGGCCAGGCACAGGAGAGAG 1598 Db 571 SerGlyProProGlnSerArgArglys 579 RESULT 4 US-09-666-421B-348 Sequence 348, Application US/09606421B Sequence 348, Application US/09606421B Sequence 348, Application US/09606421B Sequence 348, Application US/09606421B Sequence 348, Application US/09606421B Sequence 348, Application US/09606421B Sequence 348, Application US/09606421B Sequence 348, Application US/09606421B Sequence 348, Application US/09606421B Sequence 348, Application US/09606421B Sequence 348, Application US/09606421B Sequence 348, Application US/09606421B Septicant: Wangy Tongtong APPLICANT: Wangy Manay Ajun Septicant: Wangy Cary R. Septicant: Wangy Cary R. Septicant: Wangy Cary R. Septicant: Wangy Cary R. Septicant: Wangy Cary R. Septicant: Wangy Cary R. Septicant: Setting Date: 2000-06-28 SOUTHARE: PERERNICE: 210121.455C9 CURRENT FILITA DATE: RATE STATIA: DATE: RATE STATIA: STATIA: BATE STATIA: B	ignment Scores: 5.54e-161 Length: 579 ore: 1875.00 Matches: 380 rcent Similarity: 84.68 Conservative: 51 st Local Similarity: 74.66\$ Mismatches: 62 ery Match: 4 Gaps: 9 -09-270-437D-7 (1-1946) x US-09-606-421B-348 (1-579)	102 CGGGTTAGGAGCCGAAATTCAAATCCGAATATTCCACCCCAGCTCCGATGGGAAGTA	222 AGTGAGACGCCAGTGGAATGTCACCTATTCCAACCGGAGCAGAGCAGGCCATC [Qy 342 GAGCAGTAGCACAGGGACCTGAGAATGGGCGCCGAGGGGGCTTTGGCTCT 392
177 ArgGlySerSerArgGlnGlySerPro	laLeu GCGTT ::::: laMet AGGTG AGGTG i::	TIAICCCGCCCCGGGGGGGGGGGGGGGGGGGGGGGGGGGG	GITCGIAIGGITAICAICACTGGACCCCCCAITCAAGGCTCAGGGAAGAATC [1338 CACATRACGTOTSCCAGCATCACCAGCTCGACCAGCTATGGCAAAAGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT

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CGGAAGATCCGAGACATCCTGGCCCAGGTTAAGCAG---CAGCATCAGAAGGGA---CAG 1571
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                                                        GAGAACGACCAGGTCATCGTGAAAATCATCGGACATTTCTATGCCAGTCAGATGCTCAA
                                                                        CGGGTTAGGAGGCGGAAAATTCCAAATTCCGAAATTTCCACCCCAGCTCCGATGGGAAGTA
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        AACGAGTTGCAGAATTTGACGCCAGCTGAGGTGGTAGTACCAAGAGACCAGACCCTGAT
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Mismatches:
Indels:
                                                                                                                                                                                                                                    Sequence 348, Application US/09542615A
Patent No. 6518256
GEMERAL INFORMATION:
APPLICANT: Fan, Liqun
APPLICANT: Fan, Liqun
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Panger, Gary R.
APPLICANT: Panger, Gary R.
APPLICANT: Panger, Cary R.
APPLICANT: Compounds NO.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TITLE OF INVENTION: CANDERN COURSENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SEQ ID NO 348
IBNGTH: 579
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Matches:
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ORGANISM: Homo sapiens
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1302 TTCTTTGGTCCCAAGGAAGTGAAGCTGGAGACCCACATACGTGGCAGCATCAGCA [0.5	RESULT 2 US-09-643-597-348 ; Sequence 348, Application US/09643597 ; Patent No. 6426072 ; GENERAL INFORMATION: ; APPLICANT: Wang, Tongtong ; APPLICANT: Fan, Liquin	APPLICANT: Bangur, Chaitanya S. APPLICANT: Hosken, Nancy APPLICANT: Fanger, Gary R. APPLICANT: Wang, A.ilun APPLICANT: Wang, A.ilun APPLICANT: Skeiky, Yasir A.W.	; APPLICANT: Hencelson, Robert A. ; APPLICANT: McMeill, Patricia D. ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY ; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER ; FILE REFERENCE: 210.121.455211 ; CURRENT APPLICATION NUMBER: US/09/643,597	; CURRENT FILING DATE: 2000-08-21 ; NUMBER OF SEQ ID NOS: 369 ; SOFTWARE: FastSEQ for Windows Version 3.0 ; SEQ ID NO 348 ; LENGTH: 579 ; TYPE: PRT ; ORGANISM: Homo sapiens	Alignment Scores: 5.54e-161 Length: 579 Pred. No.: 1875.00 Matches: 380 Score: 1875.00 Matches: 51 Percent Similarity: 84.68 Conservative: 51 Best Local Similarity: 74.66\$ Mismatches: 62 Query Match: 4 Gaps: 9	Qy 102 CGGGTTAGGAGCCGGAAAATTCAAATTCCACCCCAGCTCCGATGGGAAGTA 161 Db 77 ArgGlnArg1leArgJvsLeuGlnIleArgAsnIleProProHisLeuGlnTrpGluVal 96 Cp 162 CTGGACAGCCTGTAGGAGAACTGAGGAACTGAGGAACTGAACACCGGAGCAACTGAACACCCGAGGAACTATTGAACACTGAGCAACTGAACACCGAGGAACTGAACACCGAGGAACTGAACACCGAGGAACCAACC
228 ACGGCAGTGGTGAATGTCACCTATTCCAACCGGGAGCAGCCAGC	08 CAGGGTCACCTGTGGCAGGGGGGGGCCCAGCCAGCAGCAAGCA	rgLeuleuValProThrGlnTyrValGlyAlaileileGlyLysGluGlyAlain GCAACATCACAAAACAGACCCAGTCCAAGATAGACGTGCATAGGAAGGA	648 ATGATCTTGGAGATTATGCATAAAGAGGCTAAGGACACCAAAACGGCTGACGAGGTTCCC	279 LeuLysileLeuAlaHisAsnanPhevalGlyArgLeulileGlyLysGluGlyArgAsn 298 768 CTGAAGAAGGTAGAGACAAAAAACGGACAAAAATCACCATCTCGTGGAGACCTT 827 [828 ACCCTTTACAACCCTGAGAGGACCATCAAGGGGGGCCATCGAGAATTGTTGCGGG 887	48 AGCTCTCACCTGATCCCTGAACCTGGACTGCTGTAGGTTTTTCCCAGCT	99 PheMetGlucccgaccagcaggacarggracaggratrarcccgcccaggcagggggeredgaggagggracaggcaggagggggggggggggggggggg

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| Sequence 2. Application US/09261855A
| Sequence 2. Application US/09261855A
| Patent No. 6255055
| GENERAL INFORMATION:
| APPLICANT: Rose, Jeffrey
| TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
| TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
| TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
| TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
| CURRENT PEDILICATION NUMBER: US/09/261,855A
| NUMBER OF SEQ ID NOS: 46
| SOFTWARE PATENT NOS: 46
| SEQ ID NO 2
| SEQ ID NO 2
| LENGTH: 577
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US-09-261-855-13

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Best Local Similarity
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- 2004 Compugen Ltd.
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US-09-542-615A-176
US-09-606-4218-176
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                                                                                                                                                                                                                                       This invention describes a novel isolated polypeptide (I) which comprising an immunogenic portion of a lung tumor protein or variant (P2) which have cytostatic activity. The polypeptides and polymocleotides are used in compositions and vaccines to inhibit the development of cancer, especially lung cancer, in a patient. Methods described in the invention can be used to monitor the progression of a cancer by carrying out the detection at subsequent time points and comparing the results from the different time points. CD4+ and/or CD8+ T-Cells isolated from a patient are treated with P2, polymucleotides encoding P2 or antigen presenting cells expressing P2 and then administered to the patient to inhibit
                                                                                                                                                     tumor
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                                                                                                                                                   Isolated polypeptide comprising an immunogenic portion of a lung protein is used for detecting and monitoring progression of lung
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123 281 143 341 163 392 183 452 200 512 220 572

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the above nucleotide sequences, or degenerate variants of the above nucleotide sequences. The composition and methods are useful in diagnosing, preventing and/or treating cancer, particularly lung cancer, in gene therapy and in vaccines. This is the amino acid sequence of a recombinant human lung tumour associated protein.
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                                   CGGAAGATCCGAGACATCCTGGCCCAGGTTAAGCAG---CAGCATCAGAAGGGA---CAG
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Durham M, Fanger GR, Vedvick
Cai F, Foy TM;
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preventing and/or treating cancer, particularly lung cancer.
                                                                                                                                                                                                                                                                                                       ., , ung cancer; gene therapy; vaccine; human; squamous cell carcinoma.
                                                                                                                                                                                                                                                                                         Recombinant human lung tumour protein L523S
                                                                                                                              1598
                                                                                                                                                        586
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04-APR-2000; 2000US-00542615.

28-JUN-2000; 2000US-0066421.

02-AUG-2000; 2000US-00630940.

21-AUG-2000; 2000US-00643597.

15-SEP-2000; 2000US-00662786.

09-OCT-2000; 2000US-00662786.
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98US-00221107.
99US-00285479.
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PD, Fanger N, Rette
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28-JUN-2001; 2001US-00897778.
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02-APR-1999;
17-DEC-1999;
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10-JAN-2000;
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                                                    -----GlySerValSerLysGlnLysPro
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                                 CGGGGTCAGCCCCGCCAGGGCTCACCTGTGGCAGCGGGGCCCCAGCCAAGCAGCAGCAA
                                                                                           GIGGACATCCCCCTTCGGCTCCTGGTGCCCCACCCAGTATGTGGGTGCCATTATTGGCAAG
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                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes isolated human lung carcinoma polymucleotides (1) and polypeptides (11). (1) and (11) have cytostatic activity, and can be used in gene therapy and in vaccines. Compositions comprising (1) or (11) can be used for stimulating an immune response in a patient and for treating lung cancer in a patient. Oligonucleotides of (1) can be used for detecting the presence of a cancer in a patient, by obtaining a biological sample from the patient, contacting the biological sample from the patient, contacting the biological sample with the oligonucleotide, detecting in the sample, an amount of polymucleotide that hybridises to the oligonucleotide and comparing the amount of polymucleotide that hybridises to the oligonucleotide to a cancer in predetermined cut-off value, and determining the presence of a cancer in the patient. (1) and (11) are useful in pharmaceutical compositions, e.g. vaccines. (1) is useful as a marker to indicate the presence or absence of a cancer such as lung cancer. ABB09145 to ABB09486 and ABP61866 to ABP61992 represent sequences used in the exemplification of the present
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                                                                                                                                                                                              Henderson RA;
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                                                                                                                                                                                                                                                                                                      Novel lung carcinoma polynucleotide sequences and polypeptides enco
the polynucleotides, useful in pharmaceutical compositions such as
vaccines and as markers to indicate the presence of lung cancer.
                                                                                                                                                                                              K, Kalos MD, Henderso
Durham M, Fanger GR,
Cai F, Foy IM;
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Matches:
Conservative:
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Retter MW, I
Peckham DW,
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07-MAY-2001; 2001US-00850716.
28-JUN-2001; 2001US-00897778.
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Mcneill PD, Fanger N,
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Query Match:
DB:
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                 WO200247534-A2
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N-PSDB; ABL49283

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The present invention describes human lung tumour proteins. Human lung activities, and can be used in vaccine production. Compositions comprising the lung tumour proteins, polymucleotides, and can be used in vaccine production. Compositions comprising the lung tumour proteins, polymucleotides, antibodies, fusion proteins, T cell populations, or antigen presenting cells that express the lung tumour proteins are useful for treating lung cancer or stimulating an immune response. ABLA8959 to ABLA9300 and ABB74946 to ABB75070 represent sequences used in the exemplification of the present
                              tumor polypeptides, useful for immune response.
                                                                                              Page 354-355; 374pp; English
                                    s encoding lung
stimulating an
                                      Polynucleotides
                                                           or
                                                           cancer
                                                                                                                                                                                                                                                                                                invention
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Sequence 586 AA;

6.2e-160 Length: 586 1875.00 Matches: 380 84.68\$ Conservative: 51 74.66\$ Mismatches: 62 53.10\$ Indels: 16 5 Gaps:) x ABB75048 (1-586)	102 CGGGTTAGGAGCCGGAAAATTCAAATCGAAATATTTCCACCCCAGCTCCGA)	ArgGlnArglleArgLysLeuGln11eArgAsn11eProProHisLeuGln1	162 CTGGACAGCCTGCTGCTGCAGTATGGTACAGTAGAGAACTGTGAGCAAGTG	104 LeuAspSerLeuLeuValGlnTyrGlyValValGluSerCysGluGlnValV	222 AGIGAGACGCAGIGGIGAAIGICACCIATICCAACGGGAGCAGACCAGGG	SerGluThrAlaValValAsnValThrTyrSerSerLysAspGlnAlaArg	282 AIGAAGCIGAAIGGCCACCAGIIGGAGAACCAIGCCCIGAAGGICICCIAC!	144 AsplysLeuAsnGlyPheGlnLeuGluAsnPheThrLeuLysValAlaTyr
Alignment Scores: Pred. No.: Score: Percent Similarity: Query Match: 55	US-09-270-437D-7 (1-1946) x ABB75048 (1-586)	Oy 102 CGGGTTAGGAG	Db 84 ArgGlnArgIl	Qy 162 CTGGACAGCCTGCTGGCTG	104 LeuAspSerLe	Qy 222 AGTGAGACGGC	Db 124 SerGluThrAl	Qy 282 ATGAAGCTGAA	Db 144 AspLysLeuAs

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Page 14

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Dest Local Similarity: 74.66\$ Mismatches: 62 Query Match: 53.10\$ Indels: 16 DB: 7 Gaps: 9 US-09-270-437D-7 (1-1946) X ADA28438 (1-579) QY 102 CGGGTTAGGAGGCGGAAATTCAAATCCGAATTATCCACCCCAGCTCCGAAGGTA 161 Db 77 ArgGlnArg1leArgLysLeuGlnIleArgAsnIleProProHisLeuGlnTrpGluVal 96 QY 162 CTGGACAGCTGGCTGGGTTAGGGAACTGTGGAAATGAGAAATGAGAAATGAAAGAAGAAGTGAAAATGAGAAATGAAAGAAAGTGAAAGAAG	Db 97 LeuAspSerLeuLeuValGinTyrGiyValValGiuSerCysGlüGinValAsnThrAsp 116 Qy 222 AGTGAGACGGCAGTGGTGAATGTCACCTATTCCAACGGGAGCAGCAGCCAGC	Db 137 Asplyslein	Db 177 ArgdlySerSerArgGlnGlySerPro		Qy 633 TCCTCCGCTTGTAAGATGATCTTGGAGATTATGCATAAGAGGCTAAGGACACCCAAACG 692 Db 254 SerAlaAlaCysLysSerIleLeuGlulleMetHisLysGluAlaGluAspIleLysPhe 273 Qy 693 GCTGACGAGGTTCCCCTGAAGATCCTGGCCCATAATAACTTTGTAGGGGGTCTCATTGGC 752 Db 274 ThrGluGluIleProLeuLysIleLeuAlaHisAsnAsnPheValGlyArgLeuIleGly 293	Qy 753 AAGGAAGGACCTGAAGAAGGTAGACATACCGAGACAAAATCACCATCTCC 812 Db 294 LysGluGlyArgAsnLeuLysLysIleGluGlnAspThrAspThrLysIleThrIleSer 313 Qy 813 TCGTTGCAAGACCTTACACCCTGAGAGACCATCACTGTGAAGGGGCCCATC 872 Db 314 ProLeuGlnGluLeuThrEeuTyrAsnProGluArgThrIleThrValLysGlyAsnVal 333	Oy 873 GAGAATTGTTGCAGGGCCGAGCAATAATGAAGAAGTTCGGGAGGCCTATGAGAAT 932	Qy 987 GGTCTTTCCCAGCTTCATCCAGCGCAGTCCCGCCGCCTCCCAGCAGCGTT 1037

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|SerAlaAlaCysLysSerIleLeuGluIleMetHisLysGluAlaGlnAspIleLysPhe
                                                                          813 TCGTTGCAAGACCTTACCTTTACAACCCTGAGAGGACCATCACTGTGAAGGGGGCCATC
                            TCCTCCGCTTGTAAGATGATCTTGGAGATTATGCATAAAGAGGCTAAGGACACCAAAAACG
                                                                 693 GCTGACGAGGTTCCCCTGAAGATCCTGGCCCATAATAACTTTGTAGGGCGTCTCATTGGC
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for diagnosing, preventing and/or treating cancer, particularly lung cancer. A new isolated polynucleotide comprises: any of the 22 fully defined nucleotide sequences (e.g. 1012, 900 or 2773 bp) given in the specification; complements of the nucleotide sequences cited above; at least 10 contiguous residues of the nucleotide sequences cited above; a sequence that hybridise to any of the nucleotide sequences under highly stringent conditions; a sequence that is at least 75 or 90% identical to the above nucleotide sequences; or degenerate variants of the above nucleotide sequences; or degenerate variants of the above nucleotide sequences; or he composition and methods are useful in diagnosing, preventing and/or treating cancer, particularly lung cancer, in gene therapy and in vaccines. This is the amino acid sequence encoded by a human lung tumour cDNA isolated from a lung squamous cell carcinomat that may be useful in the diagnosis and treatment of lung cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention describes isolated polynucleotides and polypeptides useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;
Moneill PD, Fanger N, Retter MW, Durham M, Fanger GR, Vedvick TS;
Carter D, Watanabe Y, Peckham DW, Cai F, Foy TM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotides and polypeptides useful for diagnosing, preventing and/or treating cancer, particularly lung cancer.
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                                                                                                           Human lung tumour protein L523S
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21-AUG-2000; 2000US-0064597.
15-SEP-2000; 2000US-00665597.
09-OCT-2000; 2000US-00685696.
12-DEC-2000; 2000US-00735705.
07-MAX-2001; 2001US-00897716.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-00040802.
98US-00123912.
98US-00221107.
99US-00466396.
99US-00476496.
2000US-00480884.
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2000US-00542615.
2000US-00606421.
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                                                                                                                                                                                                 lung squamous cell carcinoma
                                                     (first entry)
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02-AUG-2000; 2
21-AUG-2000; 2
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22-DEC-1998;
02-APR-1999;
17-DEC-1999;
30-DEC-1999;
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04-APR-2000;
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453 GTGGACATCCCCCTTCGGCTCCTGGTGCCCAGTATGTGGGGTGCCATTATTGGCAAG
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        CORIXA CORP.
                                                   WPI; 2003-540798/51.
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                                                                                                             CACATACGTGTGCCAGCATCAGCAGCTGGCCGGGTCCATTGGCAAAGGTGGAAAAACGGTG 1397
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                     CTCTCCCGGTTTGCCAGCGCCTCCATCAAGATTGCACCACCCGAAACACCTGACTCCAAA
                                                                                                                      gene therapy; vaccine; human;
                                                                                                                                                                                                                                                                                                                         Recombinant human lung tumour protein L5238 #2
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15-SEP-2000; 2000US-00685696.
4 12-DEC-2000; 2000US-0035705.
8 07-MAY-2001; 2001US-00897778.
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98US-00123912.
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27-JUL-1998;
22-DEC-1998;
22-APR-1999;
17-DEC-1999;
30-DEC-1999;
22-FEB-2000;
24-APR-2000;
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02-AUG-2000;
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Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Hendersor
Mcneill PD, Fanger N, Retter MW, Durham M, Fanger GR,
Carter D, Watanabe Y, Peckham DW, Cai F, Foy TM;
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Matches:
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                 US-09-270-437D-7 (1-1946) x ADA28536 (1-579)
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Retter MW, Durham M, Fanger GR, Vedvick
Peckham DW, Cai F, Foy TM;
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Mismatches:
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                                                                                    Recombinant human lung tumour protein L523S
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           Ą
         protein; 579
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99US-00466396.
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09-OCT-2000; 2000US-0068596.
12-DEC-2000; 2000US-00758705.
07-MAY-2001; 2001US-00850716.
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2000US-00510376.
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28-UTM-2000; 2000US-0066421.
02-AUG-2000; 2000US-00630940.
21-AUG-2000; 2000US-00643597.
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28-JUN-2001; 2001US-00897778.
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lung squamous cell carcinoma
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           standard;
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Best Local Similarity:
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10-JAN-2000;
22-FEB-2000;
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17-DEC-1999;
                                                            20-NOV-2003
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ADA28536
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Vedvick TS;
Durham M, Fanger GR,
Cai F, Foy TM;
 Retter MW,
Peckham DW,
 , Fanger N,
Watanabe Y,
Mcneill PD,
              Carter D,
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WPI; 2002-583465/62. N-PSDB; ABQ92483.

Novel lung carcinoma polynuclectide sequences and polypeptides encoded by the polynuclectides, useful in pharmaceutical compositions such as vaccines and as markers to indicate the presence of lung cancer.

Claim 9; Page 372-374; 381pp; English

The present invention describes isolated human lung carcinoma polymucleotides (I) and polypeptides (II). (I) and (II) have cytostatic polymucleotides (I) and polypeptides (II). (I) and (II) have cytostatic cativity, and can be used in gene therapy and in vaccines. Compositions comprising (I) or (II) can be used for stimulating an immune response in a patient and for treating lung cancer in a patient. Oligonucleotides of (I) can be used for detecting the presence of a cancer in a patient, by obtaining a biological sample trom the patient, contacting the biological sample with the oligonucleotide, detecting in the sample, an amount of camparing the patient, contacting the biological cample with the oligonucleotide that hybridises to the oligonucleotide to a mount of polynucleotide that hybridises to the oligonucleotide to a cancer in the patient. (I) and (II) are useful in pharmaceutical compositions, e.g. vaccines. (I) is useful as a marker to indicate the presence or absence of a cancer such as lung cancer. ABP02145 to AB02486 and ABP61866 to a cancer in the exemplification of the present invention

Sequence 579 AA;

579 380 51 62 16 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 6.17e-160 1875.00 84.68% 74.66% 53.10% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match: DB:

US-09-270-437D-7 (1-1946) x ABP61973 (1-579)

RESULT

 GlyThr 253	CAAAACG 692 eLysPhe 273	CATTGGC 752 uileGly 293	CATCTCC 812 rileSer 313	GCCATC 872 ::: /AsnVal 333	rgagaar 932 cGluasn 353	rgcrgra 986 ::: halaLeu 373	ZAGCGTT 1037 ::::: CAlaMet 393	3CAGGTG 1097 ::: HisLeu 410	CAAACAG 1157 SLysGln 430	_ CTCCAAA 1217 ::: OAlaLys 450	AGAATC 1277 Argile 470	3GAGACC 1337 1GluAla 490	AACGGTG 1397 sThrVal 510	CCTGAT 1457 :ProAsp 530	CAGATGGCTCAA 1517 ::: 31nValAlaGln 550		
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nger GR, Vedvick TS;
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HisIleArgValProSerPheAlaAlaGlyArgValIleGlyLysgGlyGlyLysThrVal
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Retter MW, Durham M, Fanger GR,
Peckham DW, Cai F, Foy TM;
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PD, Fanger N, Retter
), Watanabe Y, Peckham
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07-MAY-2001; 2001US-00850716.
28-JUN-2001; 2001US-00897778.
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N-PSDB; ABQ92485.
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Human; lung cancer; lung tumour; cytostatic; gene therapy; vaccine.

12-DEC-2000; 2000US-00735705. 07-MAY-2001; 2001US-00850716. 28-JUN-2001; 2001US-00897778.

30-NOV-2001; 2001WO-US047576.

WO200247534-A2

20-JUN-2002

Homo sapiens.

Human lung cancer associated protein sequence SEQ ID NO:348

(first entry)

07-OCT-2002

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GlyLeuPheProProThrSerGlyMetProProProThrSerGlyProProSerAlaMet 393
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CACATACGTGTGCCAGCATCAGCTGGCCGGGTCATTGGCAAAGGTGGAAAAACGGTG
                                AAGGAAGGACGGAACCTGAAGAAGGTAGAGCAAGATACCGAGACAAAAATCACCATCTCC
                                                                                 813 TCGTTGCAAGACCTTACCCTTTACAACCCTGAGAGGACCATCACTGTGAAGGGGGCCATC
                       GCTGACGAGGTTCCCCTGAAGATCCTGGCCCATAATAACTTTGTAGGGCGTCTCATTGGC
                                                                                                                GAGAATTGTTGCAGGCCCGAGCAGGAAATAATGAAGAAAGTTCGGGAGGCCTATGAGAAT
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The present invention describes isolated human lung carcinoma cativity, and can be used in gene therapy and in vaccines. Compositions computising (1) or (11) can be used for stimulating an immune response in comprising (1) or (11) can be used for stimulating an immune response in comprising (1) or (11) can be used for stimulating an immune response in a patient and for treating lung cancer in a patient. Oligonucleotides of containing a biological sample the presence of a cancer in a patient, by cobtaining a biological sample from the patient, contacting the biological sample with the oligonucleotide, detecting in the sample, an amount of polynucleotide that hybriddises to the oligonucleotide and comparing the amount of polynucleotide that hybriddises to the oligonucleotide to a cancer in predetermined cut-off value, and determining the presence of a cancer in corrections. (1) and (11) are useful in pharmaceutical compositions, e.g. vaccines. (1) is useful as a marker to indicate the presence or absence of a cancer such as lung cancer. AB092145 to AB092486 and ABP61866 to the contained or the present sequences used in the exemplification of the present
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                                               Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;
Mcneill PD, Panger N, Retter MW, Durham M, Fanger GR, Vedvick TS;
Carter D, Watanabe Y, Peckham DW, Cai F, Foy TM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGTGAGACGCCAGTGGTGAATGTCACCTATTCCAACCGGGAGCAGACCAGGCAAGCCATC
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                                                                                                                                                                                                                                                     Novel lung carcinoma polynucleotide sequences and polypeptides enconthe polynucleotides, useful in pharmaceutical compositions such as vaccines and as markers to indicate the presence of lung cancer.
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16
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Matches:
Conservative:
Mismatches:
Indels:
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84.68%
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(CORI-) CORIXA CORP.
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N-PSDB; ABQ92440.
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117

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standard; protein; 579

ABP61917 ABP61917;

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TCCTCCGCTTGTAAGATGATCTTGGAGATTATGCATAAAGAGGCTAAGGACACCAAAACG
                                                PD, Fanger N,
TS, Carter D,
                                                                                                 2002-090513/12.
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Query Match:
DB:
                                 Wang A,
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Mcneill
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tumour; lung cancer; cytostatic; immunostimulant; vaccine;
                    ||| ||| ||| ||| ||| ||| Thr----ProProTyrProGlnPheGluGlnSer---GluThrGluThrValHisLeu
                                                                                                                                                                                                  CTCTCCCGGTTTGCCAGCGCCTCCATCAAGATTGCACCACCCGAAACACCTGACTCCAAA
                                                                                                                                                                                                                                                                  GTTCGTATGGTTATCATCACTGGACCGCCAGAGGCCCCAATTCAAGGCTCAGGGAAGAATC
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                                                                  ACTGGGGCTGCTCCCTATAGCTCCTTTATGCAGGCTCCCGAGGAGATGGTGCAGGTG
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GGTCTTTTCCCAGCTTCATCCAGCGCAGTCCCGCCG
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2000US-00630940.
2000US-0065297.
2000US-00662786.
2000US-00685696.
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21-AUG-2000;
15-SEP-2000;
09-OCT-2000;
12-DEC-2000;
07-MAY-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
                                                                                                                                                                   GluAsnAspGlnValValValValLysIleThrGlyHisPheTyrAlaCysGlnValAlaGln
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Vedvick TS, Carter D, Watanabe Y, Peckham DW;
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|SerGlyProProGlnSerArgArgLys 579
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; 2000US-00643597.
; 2000US-0062786.
; 2000US-00685696.
; 2000US-00735705.
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21-AUG-2000;
15-SEP-2000;
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GGICTITICCCAGCTICAICCAGCGCAGTCCCGCCG------CCTCCCAGCAGCGTT 1037
   SerGluThrAlaValValAsnValThrTyrSerSerLysAspGlnAlaArgGlnAlaLeu 136
                                         ArgGlySerSerArgGlnGlySerPro-----GlySerValSerLysGlnLysPro 193
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| GluThrAlaAlaGlnGlnAsnProLeuGlnGlnProArgGlyArgArgGlyLeuGlyGln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes human lung tumour proteins. Human lung activaties, and can be used in vaccine production. Compositions comprising the lung tumour proteins, polynucleotides, polynucleotides, antibodies, proteins, T cell populations, or antigen presenting cells that express the lung tumour proteins are useful for treating lung cancer or stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to ABB75070 represent sequences used in the exemplification of the present
                                                                                                lung cancer; cytostatic; immunostimulant; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGGGTTAGGAGCCGGAAAATTCCGAAATATTCCACCCCAGCTCCGATGGGAAGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                               treating
                                                                       Human lung tumour L523S recombinant protein sequence SEQ ID NO:446
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                                                                                                                                                                                                                                                                                                                                                           Henderson RJ
Fanger GR;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Polynucleotides encoding lung tumor polypeptides, useful for lung cancer or stimulating an immune response.
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Marnerakis M,
Peckham DW;
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                                                                                                                                                                                                                                                                                                                                                        Wang T, Wang A, Skeiky YAW, Li SX,
Mcneill PD, Fanger N, Retter MW, M
Vedvick TS, Carter D, Watanabe Y,
  AA
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02-ANG-2000; 2000US-00630940.

21-AUG-2000; 2000US-00643597.

15-SEP-2000; 2000US-00662786.

09-OCT-2000; 2000US-00685696.

12-DEC-2000; 2000US-0075705.

07-MAY-2001; 2001US-00850716.
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Percent Similarity:
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                                                                                               Human, lung tum
immune response
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Isolated polypeptide comprising an immunogenic portion of a lung protein is used for detecting and monitoring progression of lung
                                                                                                      Claim 3; Page 259-261; 261pp; English.
10-JAN-2000; 2000US-00480884.
22-FEB-2000; 2000US-00510376.
                                                   2000-628399/60.
                      CORIXA CORP
                                                   WPI; 2000-628399
N-PSDB; AAC66035
                                     Fan L;
                                                                                        in a patient
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                      (CORI-)
                                     Wang
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tumor

This invention describes a novel isolated polypeptide (I) which comprising an immunogenic portion of a lung tumor protein or variant (P2) which have eytoetatic activity. The polypeptides and polynucleotides are used in compositions and vaccines to inhibit the development of cancer, especially lung cancer, in a patient. Methods described in the invention can be used to monitor the progression of a cancer by carrying out the detection at subsequent time points and comparing the results from the different time points. CD4+ and/or CD8+ T-Cells isolated from a patient are treated with P2, polynucleotides encoding P2 or antigen presenting calls expressing P2 and then administered to the patient to inhibit development of cancer

Sequence 579 AA

		161	96	221	116	281	136	341	156	392	176	452	193	512	213	572	233	632
Length: 579 Matches: 380 Conservative: 51 Mismatches: 62 Indels: 16 Gaps: 9	-579)	CCGAAATATTCCACCCCAGCTCCGATGGGAAGTA 1		CTGGACAGCCTGCTGGTCAGTATGGTACAGTAGAGAACTGTGAGCAAGTGAACACCGAG 2		TTCCAACCGGGAGCAGCCAGGCAAGCCATC	GlnAlaArgGlnAlaLeu	ATGAAGCTGAATGGCCACCAGTTGGAGAACCATGCCCTGAAGGTCTCCTACATCCCCGAT 3	AspLysLeuAsnGlyPheGlnLeuGluAsnPheThrLeuLysValAlaTyrIleProAsp	CAGGGACCTGAGAATGGGCGCCGAGGGGCTTTGGCTCT	 GluThrAlaAlaGlnGlnAsnProLeuGlnGlnProArgGlyArgArgGlyLeuGlyGln	CACCTGTGGCAGCGGGCCCCAGCCAAGCAGCAGCAA 4	GlySerValSerLysGlnLysPro	CAGTATGTGGGTGCCATTATTGGCAAG	/alGlyAlaileileGlyLys	GAGGGGCCACCATCCGCAACATCACAAAACAGACCCAGTCCAAGATAGACGTGCATAGG	LysGlnThrGlnSerLysIleAspValHisArg	AAGGAGAACGCAGGTGCAGCTGAAAAAGCCATCAGTGTGCACTCCACCCCTGAGGGCTGC (
09	AAB11365 (1-5'	CGGGTTAGGAGCCGGAAAATTCAAATC		TCAGTATGGT	lGlnTyrGly	AGTGAGACGGCAGTGGTGAATGTCACCTA	lvalAsnvalThr	ACCAGTTGGAG	 eGlnLeuGlu	AGGGACCTGAG	In InAsnProLeu	뒨=	 ArgGlySerSerArgGlnGlySerPro	GTGGACATCCCCTTTCGGCTCCTGGTGCCCACO	rgLeuLeuVal	SCAACATCACA	eArgAsnlleThr	CAGCTGAAAAA
6.17e-1 1875.00 84.68% 74.66% 53.10%	×	GAGCCGGA	 ArgGlnArgIleArgLysLeuGlnI	CCTGCTGG		GGCAGTGG	laVa 1	GAATGGCC		Ì	laAlaGlnG	CGGGGTCAGCCCCGCCAGGG	 srSerArgG	CCCCCTTC	LeuProLeuA	CACCATCO		ACGCAGGTG
cores: ilarity: Similarity:	0-7 (1-1946)	-		_	LeuAspSe		SerGluThrA			GAGCAGATAGCA		-				_	GluGlyAlaThri	
ent S No.: t Sim ocal Match	-270-437D-7	102	77	162	76	222	117	282	137	342	157	393	177	453	194	513	214	573
Alignment Pred. No. Score: Percent S Best Loca Query Mat	0-SD	à	qa	οy	qa	δy	QQ	QY	qq	δλ	qa	70	DP	δχ	qq	Qy	qa	ò

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RESULT 3

1397 1457 1517 1217 1337 1571 1037 1097 1157 1277 510 530 550 410 430 450 470 490 570 872 333 932 986 373 393 812 313 353 692 273 752 293 TCGTTGCAAGACCTTACCCTTTACAACCCTGAGAGGACCATCACTGTGAAGGGGGCCATC ACTEGGGCTGCTCCCTATAGCTCCTTTATGCAGGCTCCCGAGCAGGAGATGGTGCAGGTG 394 Thr -----ProprotyrProGlnPheGludinSer---GluThrGluThrValHisLeu CTCTCCCGGTTTGCCAGCGCCTCCATCAAGATTGCACCACCGAAACACCTGACTCCAAA TATGGCAAACTCAAGGAGAACTTCTTTGGTCCCAAGGAGGAAGTGAAGCTGGAGACC GAGAACGACCAGGTCATCGTGAAAATCATCGGACATTTCTATGCCAGTCAGATGGCTCAA CGGAAGATCCGAGACATCCTGGCCCAGGTTAAGCAG----CAGCATCAGAAGGGA---CAG GATGTGGCTGCCATGAGC----TCTCACCTGATCCCTGGCCTGAACCTGGCTGCTGTA |||||||||||| :::||| GlyLeuPheProProThrSerGlyMetProProProThrSerGlyProProSerAlaMet TTTATCCCCCCCAGGCAGTGGGCGCCATCATCGGCAAGAAGGGGCCACATCAAACAG GITCGIATGGITATCATCACTGGACCGCCAGAGGCCCCAATTCAAGGCTCAGGGAAGAATC CACATACGTGTGCCAGCATCAGCAGCTGGCCGGTCATTGGCAAAAGGTGGAAAAACGGTG 1398 AACGAGTIGCAGAATITIGACGGCAGCIGAGGIGGIAGIACCAAGAGAGACCCAGAT **AAGGAAGGACGGAACCTGAAGAAGGTAGAGCAAGATACCGAGACAAAAATCACCATCTCC** TCCTCCGCTTGTAAGATGTTTGGAGATTTATGCATAAAGAGGCTAAGGACACAAAACG ThrgluglulleProLeuLysIleLeuAlaHisAsnAsnPheValGlyArgLeulleGly GAGAATTGTTGCAGGCCGAGCAGGAAATAATGAAGAAAGTTCGGGAGGCCTATGAGAAT -CCTCCCAGCAGCGTT GCTGACGAGGTTCCCCTGAAGATCCTGGCCCATAATAACTTTGTAGGGCGTCTCATTGGC GGICTITICCCCAGCTICATCCAGCGCAGTCCCGCCG AGTAACCAGGCCCAGGCACGGAAG 1598 411 1278 1338 491 1458 531 1518 551 1098 1038 1158 1218 254 693 274 294 813 873 334 933 354 987 374 633 753 g 셤 g g à ਨੋ q à d Db g ò qq ò g ò g à g à g ₽ 셤 ð à à ð a δ g δ ò 8

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30-DEC-1999;
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                          The present sequence represents a murine c-myc coding region determinant binding protein (CRD-BP). The presence or absence of a tumor can be determined by determining the levels of CRD-BP present in the suspect tissue, where the CRD-BP shields c-myc RNA from endonucleolytic attack and so prolongs its half-life. The methods are used for diagnosing presence or absence of a tumor in a human, especially breast, colon and pancreatic cancer. They are also used to inhibit cancer cell growth
                                                                                                                                                                                                                                                                                                                                                  ThralavalvalvalasnvalThrTyrSerAsnArgGluGlnThrArgGlnAlaIleMetLys
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                          AlaGluGlnGluIleMetLysLysValArgGluAlaTyrGluAsnAspValAlaAlaMet
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   Command line parameters:

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-Q=/cgn2_1/USFTO_spool_p/US09270437/runat_23072004_095738_27403/app_query.fasta_1.5582
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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12875.302 Million cell updates/sec
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Abb75054 Human
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                    GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                    - protein search, using frame_plus_n2p model
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Maximum Match 100%
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1. geneseqp1980s:*

2. geneseqp1990s:*

3. geneseqp2001s:*

5. geneseqp2013s:*

5. geneseqp203s:*

7. geneseqp203s:*

7. geneseqp203s:*
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Score

Result

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Database

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/clone_lib="NIH_MGC_88"
/note="Organ: small intestine; Vector: pCMV-SPORTE;
/note="Organ: small intestine; Vector: pCMV-SPORTE;
/note="Not1; Site_2: Sall; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full.length clones and constructed by Life
Technologies. Note: this is a NIH_MGC Library."
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34.0%; Score 662; DB 10; Length 896;
Best Local Similarity 93.4%; Pred. No. 1.8e-156;
Matches 727; Conservative 0; Mismatches 40; Indels 1.
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Search completed: July 24, 2004, 16:42:21 Job time : 4881.33 secs

563 300 623 360 683 420 743 480 803

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BF984962 896 bp mRNA linear EST 23-JAN-2001
602308484F1 NIH_MGC_B8 Homo sapiens cDNA clone IMAGE:4399556 5',
mRNA sequence.
BF984962
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: gapba-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arzayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Theyte Genomics, Inc.
clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:
http://mage.lnl.gov
Plate: LiAMN10103 row: h column: 21
High quality sequence stop: 652.
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                                                                                                                                                                                                                                                                                              GAGGGCTGCTCCCCTTGTAAGATGATCTTGGAGATTATGCATAAAGAGGCTAAAGGAC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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AGENCOURT_8297761 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6269842
5', mRNA sequence.
BQ651665.1 GI:21775837
                                                                                                                    NTGCCCCTCGGGGTGTCAGAAATINTAGCGCAAGGCACTTTTAAACGTGGATTGTTAAA 1868
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 955)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-remail.nih.gov
Tissue Procurement: CGAP (Stanford)

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:

http://image.llni.gov

Plate: LLCM2444 row: a column: 11

High quality sequence stop: 588.
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                                                                        541 CTGCCCCTGGGGGTGTCAGAAATTCTAGCGCAAGGCACTTTTAAAAGGGGATGTTTAAA
                                                                                                                                         THI-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Pred. No. 1.7e-156;
0; Mismatches 8; Indels 0;
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/organism="Homo sapiens"
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. I (bases 1 to 712)
11 HMGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

GI:20406982

BQ225582.1 EST.

Homo sapiens (human)

þe

Mon

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Context: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13225 row: j column: 06
High quality sequence stop: 625.
Location/Qualifiers
                                           ORGANISM
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1. 712
/ organism="Homo sapiens"
/ organism="Homo sapiens"
/ mol_type="mRNA"
/ db_xref="taxon:9606"
/ clone="!MAGE:6020837"
/ tissue_type="epithelioid carcinoma"
/ lab host="lablo08 (phage-resistant)"
/ clone="lib="NIH MGC_70"
/ note="organ: pancreas, Vector: pCMV-SPORT6; Site 1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.1 kb. Library constructed by Life
Technologies."
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Local Similarity 99.3%; Pred. No. 2.7e-158; ies 669; Conservative 0; Mismatches 5;
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AGENCOURT 7593363 NIH MGC_70 Homo sapiens cDNA clone IMAGE:6020837 BQ225582

BQ225582 LOCUS DEFINITION

ACCESSION

RESULT 13

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1776

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BX401619
BX401619 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED Homo sapiens cDNA clone CS0DL005YL19 3-PRIME, mRNA sequence.
BX401619
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BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 0100 of Invitogen. This sequence belongs to sequence cluster
BP 191 For more information about this cluster, see
Http://www.genoscope.cns.fr/
BP 191 01005CF10NP1&Cluster=8942.f. Contact :
Feng Liang Enail: fliang@lifetech.com URL :
Http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODLOOSCF10NP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              660 GAICAGGITIGCC--ACTIGAIGAGAAAGAIGTICCAGIGAGGAACCCIGAICTCIAGCC 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mark" | for the following primer | for the following primer | for the for the for the for the for the for the for the for the for the for the for the for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the for the for the for the for the for the for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the form | for the
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1 (bases 1 to 1201)

1 (hases 1 to 1201)

Full, M.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

Contact: Genoscope
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                                                                                                                                                                                                                1538 GGCCCAGGTTAAGCAGCAGCATCAGAAGGGACAGAGTAACCAGGCCCCAGGCACGAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               540 GTGACCAGCCCTCCCTGTCCCTTCGAGGACAGGACAACGGGCAGAAATCGAGAGG
361 GGCAGCTGAGGTAGTACCAAGAGACCAGACCCCTGATGAGAACGACCAGGTCATCGT
                                                                                                                                   421 GAAAATCATCGGACATTTCTATGCCAGTCAGATGGCTCAACGGAAGATCCGAGACATCCT
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    .1201
    /organism="Homo sapiens"

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84.6%;
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGGACCGCCAGAGGCCCCAATTCAAGGCTCAGGGAAGAATCTATGGCAAACTCAAGGAGGA
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                                                                                    BG115319 831 bp mRNA linear EST 30-JAN-602316274F1 NIH_MGC_B8 Homo sapiens cDNA clone IMAGE:4416354 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.W.A.G.E. Consortium/Link at:
http://mage.llnl.gov.d column: 19
Plate: LiAM10147 row: d column: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 831)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 731.
Location/Qualifiers
                                                                                                                                                                                                            BG115319
BG115319.1 GI:12608825
                                                                                                                                                                                                                                                                                                                        Homo sapiens (human)
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                                                                                                                                                                             mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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BG115319
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/clone_lib="NIH_MGC_100"
hote="Organ: liver; Vector: pOTB7; Site 1: Xho1; Site 2: EcoR1; cDNA made by oligo-dT priming brectionally cloned into EcoR1/Xho1 sites using the following 5; adaptor: edgcAcGAGG(G). Size-selected >500pp for average insert size 1: 8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript Library."
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Pred. No. 1.1e-160;
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5', mRNA Sequence.
                                                                                                                                                                                                                         TCATCACTGGACCGCCAGGGCCCAATTCAAGGCTCAGGGAAGAATCTATGGCAAACTCA 1290
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/lab_host="DH10B (phage-resistant)"
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                                                                                    AGGCAGTGGGCGCCATCATCGGCAAGAAGGGGCAGCACATCAAACAGCTCTCC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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/db_xref="taxon:9606"
/clone="IMAGE:6284231"
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/organism="Homo
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LTPPYPQFEGSETETVHLF1PALSVGA1IGKQGQH1KQLSRFAGASIKIAPAEAPDAK
VRMVIITGPPEAQFKAQGRIYGKIKEENFVSPKEEVKLEAHIRVPSFAAGRVIGKGGK
TVNELQSLSSAEVVVPRDQTPDENDQVVVKITGHFYACQVAQRKIQEILTQVKQHQQQ
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_sftage="10 days embryo"
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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023670,
                                                                             FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection
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Fax:81-45-503-9216)
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Mus musculus 10 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2610036B18 product:insulin-like growth factor 2, binding protein 3, full insert sequence.
AK011689.1 GI:12847972
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/tissue type="NEUROBLASTOMA COT 25-NORMALIZED"
/tissue type="NEUROBLASTOMA COT 25-NORMALIZED"
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Catarrhini, Hominidae, Homo.
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BP 191 91006 EVRY cedex - France
BRail: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 8684.r For
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cgi-bin/cluster.cgi?seq=CSOBAG007ZH09 CS00648 l&cluster=8684.r.
cgi-bin/cluster.cgi?seq=CSOBAG007ZH09 CS00648 l&cluster=8684.r.
contact: Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOBAG007ZH09 CS00648 l.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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Mammalia; Eutheria; Primates;
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ITTEPPYPOFEGSETETYTHEFTPALSVAIIGKGOGHIKQLSRFAGASIKIAAPABADAK

VRWVIITGPPPAGGSETETYTHEFTPALSVAAIIGKGOGHIKQLSRFAGASIKIAAPABADAK

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Corganism="Mus musculus"

/mol Ltype="mkNa"

/strain="NOD"

/db_xref="TexnToM DB:E430018F06"

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                                                                                    prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
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              Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed t
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                                                                                                                                                                                                                                              Please visit our web site for further details. URL:http://genome.gsc.riken.go.jp/.URL:http://fantom.gsc.riken.go.jp/.Location/Qualifiers
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The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

E (bases I to 4100)

B Adachi, J., Aizawa, K., Akimura, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hiramoto, K., Hiraoka, T., Harozane, T., Hayashi, M., Kojima, Y., Kondo, S., Konno, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Nakaui, J., Makaura, M., Nishi, K., Nomura, R., Miyazaki, R., Ohno, M., Ohasto, N., Okazaki, Y., Saito, R., Saito, H., Sakai, C., Sakai, K., Sakzume, N., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Tanaka, T., Tanaka, T., Tanaka, T., Tanaka, T., Tanaka, T., Tanaka, T., Tomaru, M., Toya, T., Yasunishi, A., Phinas, S., Phinasaki, Y., Tanaka, T., Tomaru, N., Toya, T., Yasunishi, A., Phinasaki, Y., Tanaka, T., Tomaru, N., Toya, T., Yasunishi, A., Phinasaki, Y., Tanaka, Y., Tayaka, ARNUBR465

Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN

full-length enriched library, clone:E430018F06 product:insulin-like
growth factor 2, binding protein 3, full insert sequence.

AKOR8465 genes Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, Chordata, Craniata, Vertebrata, Buteleostomi, Rodentia, Sciurognathi, Muridae, Murinae, Mus. Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P. Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,B., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length to CDNA libraries for rapid discovery of new Genome Res. 10 (10), 1617-1630 (2000) The RIKEN Genome Exploration Research Group Phase II Team and URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Functional annotation of a full-length mouse cDNA cloning Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA Meth. Enzymol. 303, 19-44 (1999) 99279253 AKO88465.1 GI:26353479 HTC; CAP trapper. Mus musculus (house mouse) Nature 409, 685-690 (2001) Mammalia; Eutheria; Eukaryota; Metazoa; Fax:81-45-503-9216) FANTOM Consortium. Direct Submission COMMENT

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/ OLGALISHE "MENDA"

/ MOLE TYPE="MENDA"

/ MD. TYPE="MENDA"

/ Clone="INAGE-6668020"

/ Clone="INAGE-6668020"

/ Lissue type="hepetocellular carcinoma, cell line"

/ Lissue type="hepetocellular carcinoma, cell line"

/ Lissue type="hepetocellular carcinoma, cell line"

/ Lib host="Menda"

/ Lib host="Menda"

/ Clone lib="NHH MGC_100"

/ Clone lib="NHH MGC_100"

/ Note="Organ: liver; Vector: priming: Directionally cloned

into EcoRI; cDNA made by oligo-dT priming: Directionally cloned

into EcoRI; cDNA made by oligo-dT priming: Directionally cloned

into EcoRI; CDNA constructed by Ling Hong in the laboratory

of Gerald M. Rubin (University of California, Berkeley)

using ZAP-CDNA synthesis kit (Stratagene) and Superscript

II RT (Life Technologies). Note: this is a NHH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BQ648383 950 bp mRNA linear EST 15-JUL-2002
AGENCOURT_8342265 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6268202
5', mRNA sequence.
BQ648383
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NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbe-r@mail.nih.gov
Tissue Procurement: CGAP (Stanford)
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://inage.llnl.gov
Plate: LLCM2439 row: m column: 03
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 950)
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/note="Organ: eye; Vector: pCWV-SPORT6; Site_1: NotI;
/note="Organ: eye; Vector: pCWV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Library constructed by Life
Technologies."
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                             Euteleostomi;
                                                                                                                                               Context: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Trissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencout Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12263 row: 1 column: 24
High quality sequence stop: 682.
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        Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1042)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="INAGE:5550887"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/lab_host="NHH MGC 67"
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Pred. No. 1.2e-198;
0; Mismatches 18;
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/organism="Homo sapiens"
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Best Local Similarity 96.8%;
Matches 920; Conservative
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AGENCOURT_6566228 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:5550887
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/lab host="MulloB (phage-resistant)"
/clone_lib="NIH_0B (phage-resistant)"
/clone_lib="NIH_MGC_lob"
/note="Organ: liver; Vector: pOTB7; Site_1: XhoJ; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGACGAGGG; Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
                                                                       AGTICGIAIGGITATCATCAC--IGGACCGCCAGAGGCCCCAATTCAAGGCTCAGGGAAGA 1274
                                                                                                           AGTICGAAIGGITAICCAIACCIGGAACGCCCAAAGGCCCAAIICCAGGGTCAGGGAAA 1020
                                                                                                                                           ATCTATGGCAAACTCAAGGAGAAACTTCTTTGGTCCCAAGGAGGAAGTGAAGCTGGAG 1334
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                                                                                                                                                                                                                                                                                                                                               mRNA linear EST 12-MAR-2002 sapiens cDNA clone IMAGE:5797961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-remail.nih.gov
Tissue Procurement: CGAP (Stanford)
CDNA Library Pregaration: Rubin Laboratory
CDNA Library Pagaration: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2025 row: c column: 18
High quality sequence stop: 662.
I. .1042
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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GCTCTCCCGGTTTGCCAGCGCCTCCATCAAGATTGCACCACCCGAAACACCTGACTCCAA
                              GCTCTCCCGGTTTGCCCAGGCCTTCCTCAAGATTGCACACCCGGAAACACCCGGGACTCCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5797961"
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Matches 988;
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/tissue_type="hepatocellular carcinoma, cell line"
/lab host="DHIOB (phage-resistant)"
/lab host="DHIOB (phage-resistant)"
/loche=lib="NIH MGC | Tiver; Vector: pOTB7; Site_1: XhoI; Site_2: /note="Organ: liver; Vector: poTB7; Site_1: xhoI; cDNA made by oligo-dT priming. Directionally cloned
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

I (bases 1 to 1085)
NHH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CGAP (Stanford)
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
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Catarrhini; Hominidae; Homo.
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ATCATCGGACATTTCTATGCCAGCCAGATGGCTCAGCGGAAGATCCGAGACATCCTGGCT
                                                     2013 CCCCCCCCCCTCTGTCCCATGGCTCCAAGATCAGCAGGAGGAACACAGAACTGGAGGG
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                                    CAGGITAAGCAGCATCAGAAGGGACAGAGTAACCAGGCCCAGGCACGGAGGAAGTGA
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AGENCOURT 7186901 NIH_MGC_100 Homo
5', mRNA Sequence.
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Location/Qualifiers
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/db_xref="taxon:9606"
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into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC
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                                                                                                                                           13;
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                                                                                                                                        49.8%; Score 969.4; DB 13
llarity 95.3%; Pred. No. 2.1e-234;
Conservative 0; Mismatches 42;
                                                                                               Library."
                                                                                                                                                             Similarity
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Matches 1033;
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URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
pax:81-45-503-9216)
Please visit our web site (http://genome.gsc.riken.go.jp/)
further details.
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Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="13 days embryo"
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2306 TITATAA 2312	AK013940 2780 bp mRNA linear HTC 20-SEP-2003 Mus musculus 13 days embryo head cDNA, RIKEN full-length enriched	<pre>library, clone:311001023 product:insulin-like glowin raccor 2, binding protein 1, full insert sequence. AK013940.1 GI:12851513</pre>	HTC; CAP trapper. Mus musculus (house mouse) Mus musculus Eukaryota; Metazoa; Chordata;	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 Carninci,P. and Hayashizaki,Y. High-efficiency full-lenath cDNA cloning	Meth. Enzymol. 303, 19-44 (1999) 99279253 10349636	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper selected cDNAs to premare full length chan in invaries for rapid discovery of new genes	Genome Res. 10 (10), 1617-1630 (2000) 20499374 11042159	Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Vanamoro M. Matemoro M. Sakamohi,S. Itkedami,T., Kashiwadi,K.,	fullimitute, increment	Alban illegiaca sequencing pipeline with 1844 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000) 20530913	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.	Functional annotation of a full-rength mouse that correction Nature 409, 685-690 (2001) S The FANTOM Consortium and the RIKEN Genome Exploration Research	Group Phase I w 11 Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs I Nature 420, 563-573 (2002)	b (Loases 1.0 2/00, Adahira,S., Akimura,T., Arai,A., Aono,H., Adachi,J., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y., Arakawa,T., Bono,H., Hara,A., Hayatsu,N., Hiramoto,K., Harangaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Hiramoto,R., Hir	Kasukawa,T., Kato,H., Kawati,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C.,	Salbata, K., Shibata, Y., Shihagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tagami, M., Yamamura, T., Yasunishi, A., Yoshida, K., Voshida, M., Wanamara, M., And Havashi, Zaki, Y.	Direct Submission Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Fryncherion Desearch Grown, BYKEN Genomic Sciences Center (GSC),	EXPLOIATION RESEALCH GLOUP, ALLEN GENOALD CLEUCES GROOT, RIKEN YOKOhama, Institute; 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
Dp 5	RESULT 2 AK013940 LOCUS DEFINITION	ACCESSION VERSION	KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITIE	JOURNAL MEDLINE PUBBED	AUTHORS TITLE	JOURNAL MEDLINE PUBMED	AUTHORS	E	JOURNAL MEDLINE PITEMEN	REFERENCE AUTHORS	TITLE JOURNAL REFERENCE AUTHORS	TITLE	REFERENCE AUTHORS			TITLE JOURNAL	
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                                 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. SIXEN integrated sequence analysis (RISA) system--384-format Genome Res. 10 (11), 1757-1771 (2000)
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2718)
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Issues were provided by Dr. Tomohiro Kono (Department of Animal
Science, Tokyo University of Agriculture, 1737 Hunako Atsugi City,
Kanagawa Prefecture, Japan) whose assistance we gratefully
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FULLOID ADDITION Of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
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APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Fanger, Neil
TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGONOSIS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGONOSIS OF LUNG CANCER
TILLE OF INVENTION: AND DIAGONOSIS OF LUNG CANCER
TILLE OF INVENTION: AND DIAGONOSIS OF LUNG CANCER
TILLE OF INVENTION: AND DIAGONOSIS OF LUNG
CURRENT FILLING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 447

LENGTH: 1743
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Pred. No. 6.6e-200;
0; Mismatches 483;
Sequence 447, Application US/09897778
Patent No. US20020147143A1
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Marnerakis, Margarita
APPLICANT: Panger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
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Best Local Similarity 66.7%;
Matches 980; Conservative C
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1430 AAAACTTGTTAGTCCTAAAGAAGTGAAACTTGAAGCTCATATCAGAGTGCCATCCT 1489 1357 CAGCAGCTGGCGGGTCATTGGCAAAACGGGGAACGGGTTGCAGAATTTGA 146	RESULT 14 US-10-313-986-478 Sequence 478, Application US/10313986 ; Publication No. US20030236209A1 ; GENERAL INFORMATION: ; APPLICANT: Foy, Teresa M. ; APPLICANT: Matanabe, Yoshihiro ; APPLICANT: Reed, Steven G. ; APPLICANT: Reed, Steven G. ; APPLICANT: Watenabe, Yoshihiro ; APPLICANT: Nationabe, Yoshihiro ; APPLICANT: Nationabe, Yoshihiro ; APPLICANT: Nationabe, Yoshihiro ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY ; TITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER ; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER ; TITLE SETERBNCE: 210121.455019 ; CURRENT FILING DATE: 2002-12-04 ; NUMBER OF SEQ ID NOS: 560 ; SOFTWARER: RastSEQ for Windows Version 4.0 ; SEQ ID NO 478 ; LENGTH: 1740 ; TYPE: DNA ; ORGANISM: Homo sapiens	Duery Match Best Local Matches 98 103 230 222 222 350 410 440 530 590
	CCATCCGCAACATCACAAACAGCCCAAGATAGACGTGCATAGGAAACGCCATCGCAACCAAC	1010 CCAAGCCGAGCAGCACCATTACAGTTAAAGCCATGTTAAGCATTAAGCTTAAGCATGTTGGCTG 1009 883 GCAGGCCGAGCAGCAGCACCATTACAGTTAAGCTTAAGCCATGACTTGGCTG 942 1010 CCAAAGCTGAGCAGCAGCACCTGATCCGGGGGCCTATGAAATCTGGCTG 1069 1010 CCAAAGCTGAGCAGACACCTGATCCTGGCCTGACCTGTGAGTTTTTCC 996 1010 CCAAAGCTGAGCAGACATTAATCCTGGCTGACCTGTGAGTTTTTCC 1129 1010 CCAAAGCTGAGCAGTCCCGGCTTCCTGGCTTGTGGGTTTTTCC 1129 1010 CCATCATCAAGCAGTTTAATCCTGGATTAATCTGAGCTTCTGGGCTGTTTTTCC 1129 1010 CCACCTTCAAGCAGTTCCACCTCCCAGCAGCTTAATCCCGGCTTCCTTTTATCCCGGCTTTTATCCCGGCTTTTATCCCGGCTTTTATCCCGGCTTTTATCCCGGTGCTTTTATCCCGGCTTTTATCCCGGTGTTTATCCCGGTGTTTATCCCGGTGTTTATCCCGGTGTTTATCCCGGTGTTTATCCCGGTGTTTATCCCGGTGTTTATCTATGCAGAGTTTTATCCCGGTTTTATCCCGGTTTTATCCCGGTTTTATCCCGGTTTTATCCCGGTTTTATCCCGGTTTTATCCCGGTTTTATCCCGGTTTTATCCCGGTTTTATCCCGGTTTTATCTTTATCCAGCAGTTTTATCCCGGTTTTATCCCGGTTTTATCCCGGTTTTATCCCGGTTTTATCTGCTTTATCTATGCTTTATCTATGCTTTATCTATGCTTTATCTATGCTTTATCTATGCTTTATCTATGCTTTATCTATGCTTTATCTATGCTTTATCTATGCTTTATCTATGCTTTATCTATGCTTTATCTATGCTTTATCTATGCTTTATCTATGCTTTATCTATGCTTTTATGCAAAGTTTCTTTTTATGCAAAGTTTCTTTTTATGCAAAGTTTCTTTTTATGCAAAGTTTCTTTTTATGCAAAGTTTCTTTTATGGAAAGATTTCTTTTTATGAAAATTTAATGGAAAAATTAATGGAAAAATTAAAGAAAATTAAAGATTCTTTAAGATTCTCCAAGTAAAAATTAATGGAAAAATTAATGGAACCCCACACACA

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APPLICANT: Foy, Teresa M.
APPLICANT: McNabb, Andria
APPLICANT: Read, Steven G.
APPLICANT: Read, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C19
CURRENT APPLICATION NUMBER: US/10/313,986
CURRENT FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 560
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 347
LENGTH: 1740
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larity 66.7%; Pred. No. 6.6e-200;
Conservative 0; Mismatches 483;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 347, Application US/10313986; Publication No. US20030236209A1; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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                       ; TYPE: DNA
; ORGANISM: Homo
US-10-117-982-478
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Best Local Simi
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LENGTH: 1740
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APPLICANT: Menderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Spies, Gregory A.
APPLICANT: Spies, Gregory A.
APPLICANT: Spies, Gregory A.
APPLICANT: Mang, Tongerong
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C18
CURRENT FILING DATE: 2002-04-05
CURRENT FILING DATE: 2002-04-05
SOFTWARE: FastSEQ for Mindows Version 4.0
SEQ ID NO 478
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Vedvick, Thomas S.
Carter, Darrick
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US-10-117-982-478
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                                      APPLICANT: Spies, Gregory A.
APPLICANT: Fan, Liqun
APPLICANT: Fan, Liqun
APPLICANT: Wang, Tongtons
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C18
CURRENT APPLICATION NUMBER: US/10/117,982
CURRENT FILING DATE: 2002-04-05
NUMBER OF SEQ ID NOS: 484
SOFTWARE: FastSEQ for Mindows Version 4.0
SEQ ID NO 347
LENGTH: 1740
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                      Mericle, Barbara
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CRGANISM: Homo sapiens
US-10-117-982-347
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Publication No. US20030138438A1
GENERAL INFORMATION:
APPLICANT: Foy, Teresa M.
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
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Watanabe, Yoshihiro
Henderson, Robert A.
Kalos, Michael D.
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US-10-117-982-347
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Lisamual X.
APPLICANT: Lalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Rados, Nichael D.
APPLICANT: Panger, Neil
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APPLICANT: Peckman, David W.
APPLICANT: Poy, Teresa M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C17
CURRENT APPLICATION NUMBER: US/10/007,700
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FastSEQ for Windows Version 4.0
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Matches 980; Conservative
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APPLICANT: Wang, Tongtong
APPLICANT: Panger, Gary K.
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Matanabe, Yoshihiro
APPLICANT: Peckham, David W.
APPLICANT: Peckham, David W.
APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C16
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DAFE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                       TGGCCCAGGTTAAGCAGCAGCATCAGAAG 1565
                                                                                                                                                                                TGACTCAGGTAAAGCAGCACCAACAACAG 1698
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Best Local Similarity 66.7%;
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                                                                             1038 ACGIGGATIGITIAAAGAAGCICICCAAGAGCCCCAACAAGAGGIGGATCACACCICAGIG
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                                                                                                                                                                                                         Sequence 745, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: ROSEN et al.
; TILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-7
; Prior application data removed - consult PALM or file wrap; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 745
; SEQ ID NO 745
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DB
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Pred. No. 0;
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Best Local Similarity 98.7%;
Matches 1084; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
CORGANISM: Homo sapiens
US-09-764-864-745
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US-09-764-864-745
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                                                               Length 1182;
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                                                                                         Indels
                                                             DB 9;
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                                                          Score 1085.4;
Pred. No. 0;
0; Mismatches
                                                            55.8%;
                                                       Query Match
Best Local Similarity 98.9
Matches 1102; Conservative
                 sapiens
; TYPE: DNA
; ORGANISM: Homo
US-09-764-864-327
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1841 AG-GCACITITAAACGI-GGATICITIAAAGAAGCICTCCCAGCCCCACCAAGAGGGIGG 1898
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      AACAGCT---CTCCCGGTTTGCCAGCGCCTCC-ATCAAGATTGCACCACCCGAAACACCTG
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IITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ23
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrappe
NUMBER OF SEQ ID NOS: 1792
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 327
LENGTH: 1182
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                                                                                                                      ) NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040005559A1 457674.1
US-10-062-674-2082
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                                                                                                                                                                                                     Score 1291.4;
Pred. No. 0;
0; Mismatches
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Best Local Similarity 93.8%;
Matches 1621; Conservative (
                                                         TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
SOFTWARE: PERL Program
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                     SEQ ID NO 2082
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66.9%; Score 1301; DB 9; Length 2224; 6; Conservative 0; Mismatches 275; Indels 33; Gaps AGGAGCCGAAAATTCAAATCCAACCCCAAGCTCCGATGGGAAGTACTGGAC	485 ACAGCGGTGGTCACCTACTCTAACCGGGGGCCAGCCAGGCAAGCTATCATGAAG 544 288 CTGAATGGCCACCAGTTGGAGAACCATGCCCTGAAGGTCTCCTACATCAGAGG 347 [1	CAGGGCTCACCTGTGGCAGCGGGGGCCCCAGCAAGCAGCAGCAAGTGGACTCCCCCTT	528 CGCNACATCACAAACGGACCCAGTCCAAGATAGACGGAGGAGGAGGAGGAGGGGT 587 1 1 1 1 1 1 1 1 1	648 ATGATCTTGGAGATTATGCATAAAGAGGCTAAGGACACCAAAACGGCTGAGGTTCCC 707		8 GCCGAGCAGAAATAATGAAAGATATCGGGAGGCCTATGAGAATGATGTGGCTGCCATG	948 AGCTCTCACCTGATCCTGGCCTGAACCTGGTGCTGTTCCCAGCT 1001 1205 AGCTTGCCCCCCCTCGCCTGGCCTTGCTCTTCCCTTCTTCT

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Patent No. U320020061543A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
CURRENT APPLICATION NUMBER: US/09/873,637

CURRENT FILING DATE: 2001-06-04

NUMBER OF SEQ ID NOS: 46

SOFTWARE: PATENTIN Ver. 2.0

SEQ ID NO 1.
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     TTGCCAGCGCCTCCATCAAGATTGCACCACCGGAAACACCTGACTCCAAAGTTCGTATGG
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) ORGANISM: Mus musculus
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Pred. No. 0;
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PRIOR APPLICATION NUMBER: US/09/061,709
PRIOR FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 8
LENGTH: 1708
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                              Query Match
Best Local Similarity 99.8%;
Matches 1676; Conservative
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	241 ATGTCACCTATTCCAACCGGGGGGGCAAGCCATCATGAAGCTGAATGGCCACC 300	361 CTGAGAATGGGCCCGAGGGGCCTTTGGCTCTCGGGGTCAGCCCCGCCAGGGCTCACCTG 420	481 CCACCCAGTATGTGGGTGCCATTATTGGCAAGGGGGGCCACCATCCGCAACATCACAA 540	601 CCATCAGTGTGCACTCCACCCTGAGGGCTGCTTGTAAGATGATCTTGGAGA 660	GAACC	GCTGA	TCCCTGGCCTGAACCTGGTGGTGTTTTTCCCAGCTTGATCCAGCGCAGTCCGGCTTGATCCGGCTGGTGTGTGT

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(without alignments)
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| cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
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| cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO9_SUBM_PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum DB seq length: 200000000
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1946
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

		J			SUMMARIES	·
Result No.	Score	Query Match	f Query Match Length DB	DB	ID	Description
	1941	99.7	1946	9	US-09-899-651-7	Sequence 7, Appli
101	1669.2	85.8	1708	6	US-09-899-651-5	Sequence 5, Appli
m	1301	66.9	2224	6	US-09-873-637-1	Sequence 1, Appli
4	1291.4	66.4	1738	16	US-10-062-674-2082	Sequence 2082, Ap
Ŋ	1085.4	55.8	1182	6	US-09-764-864-327	Sequence 327, App
9	1069.8	55.0	1129	σ	US-09-764-864-745	Sequence 745, App
7	674.2	34.6		σ	US-09-735-705-347	Sequence 347, App
00	674.2			σ	US-09-850-716A-347	Sequence 347, App
σ	674.2			σ	US-09-897-778-347	Sequence 347, App
10	674.2			13	US-10-007-700-347	Sequence 347, App
11	674.2			15	US-10-117-982-347	
12	674.2		1740	15	US-10-117-982-478	Sequence 478, App
13	674.2			16	US-10-313-986-347	347,
14	674.2	34.6		16	US-10-313-986-478	Sequence 478, App

	7	674.2	34.6	1743	0	US-09-897-778-447	Sequence 447, App
	1 -	674.2	34.6	1743	σ	US-09-897-778-450	
	2 -	674.2	34.6	1743	13	US-10-007-700-447	447
	2	674.2	34.6	1743	13	US-10-007-700-450	Sequence 450, App
	9 0	674 2	34.6	1743	15	US-10-117-982-447	Sequence 447, App
	3 5	674.2	34.6	1743	15	US-10-117-982-450	Sequence 450, App
	2 5	674.2	34.6	1743	16	US-10-313-986-447	Sequence 447, App
	, ,	674 2	34.6	1743	16	US-10-313-986-450	Sequence 450, App
	4 C	674 2	34.6	1764	6	US-09-850-716A-428	
	4.	674.2	34.6	1764	6	US-09-897-778-428	Sequence 428, App
	, C	674.2	34.6	1764	13	US-10-007-700-428	Sequence 428, App
	20	674.2	34.6	1764	15	US-10-117-982-428	Sequence 428, App
	27	674.2	34.6	1764	16	US-10-313-986-428	Sequence 428, App
	α,	674.2	34.6	1799	16	US-10-313-986-485	Sequence 485, App
	0	674.2	34.6	34555	15	US-10-117-982-479	Sequence 479, App
	i c	674.2	34.6	34555	16	US-10-313-986-479	
	31	672.6	34.6	4159	σ	US-09-899-651-4	Sequence 4, Appli
z,	2	672.6	34.6	4181	σ	US-09-735-705-175	Sequence 175, App
	3 (672.6	34.6	4181	0	US-09-954-456-715	Sequence 715, App
	3.4	672.6	34.6	4181	σ	US-09-850-716A-175	Sequence 175, App
	3.6	672.6	34.6	4181	σ	US-09-897-778-175	Sequence 175, App
	9 (672.6	34.6	4181	10	US-09-466-396A-175	Sequence 175, App
		672.6	34.6	4181	13	3 US-10-007-700-175	Sequence 175, App
	00	672.6	34.6	4181	15	US-10-117-982-175	Sequence 175, App
	6	672.6	34.6	4181	16	US-10-313-986-175	Sequence 175, App
	0 4	672.6	34.6	4434	13	US-10-116-802-145	Sequence 145, App
	4	664.6	34.2	1740	15	US-10-117-982-483	Sequence 483, App
,	4.2	664.6	34.2	1740	16	US-10-313-986-483	Sequence 483, App
	43	585.4	30.1	3283	σ	US-09-899-651-8	Sequence 8, Appli
	44	585.4	30.1	3667	15	US-10-097-340-146	Sequence 146, App
	45	585.4	30.1	3667	17	US-10-648-593-48	Sequence 48, Appl

ALIGNMENTS

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APPLICANT: Chen, Ali
APPLICANT: Chen, Ali
APPLICANT: Tsang, Solam
APPLICANT: Tsang, Solam
APPLICANT: Stockert, Elisabeth
APPLICANT: Stockert, Elisabeth
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100.0%; Pred. No. 0;
iive 0; Mismatches
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PRIOR FILING DATE: 1998-04.7
                     Sequence 7, Application US/09899651 Patent No. US20020111470A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER: US/
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 1946; Conservative
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1683 GCTGAAGCAGCAGCAGAAATACCCTCAGGGAGTCGCCTCACAGCGCAGCAAGTGAGG 1742

1604 AGCCC 1608 |||| 1743 CTCCC 1747

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Search completed: July 24, 2004, 16:48:13 Job time : 143.138 secs

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	RESULT 15 US-09-061-709-8 US-09-061-709-8 Sequence 8, Application US/09061709B Patent No. 6297364 GREREAL INFORMATION: APPLICANT: Gure, Ali APPLICANT: Stockert, Elisabeth APPLICANT: Stockert, Elisabeth APPLICANT: Jager, Elke APPLICANT: Maxander APPLICANT: Old, Lloyd 1. APPLICANT: Old, Lloyd 1. APPLICANT: Old, Lloyd 1. APPLICANT: Old, Lloyd 1. APPLICANT: Old, Lloyd 1. APPLICANT: Old, Lloyd 1. APPLICANT: Old, Lloyd 1. APPLICANT: Old, Lloyd 1. APPLICANT: Old, Lloyd 1. APPLICANT: Old, Lloyd 1. APPLICANT: ON ENGRET APPLICATION NUMBER: US/09/061,709B CURRENT APPLICATION NUMBER: US/09/061,709B CURRENT APPLICATION NUMBER: US/09/061,709B LENGTH: 3283 TYPE: DNA ORGANISM: Homo sapiens FEATURE: US-09-061-709-8	Query Match 30.1%; Score 585.4; DB 3; Length 3283; Best Local Similarity 64.1%; Pred. No. 1.4e-160; Indels 60; Gaps 3; Matches 964; Conservative 0; Mismatches 481; Indels 60; Gaps 3; QY 104 GGTTAGGAGCGGAAATTCAGATGCGAATATTCCACCCCAGCTCGAGGGAGTT 362 Db 303 GCTAAGGAGCAGAAATTCAGATGAGAACTGTGAGCAAGTCAACACGAGACT 362 QY 164 GGACAGCCTGGCTGGTATGGTAGACAGTGGAACTGTGGAACAGCAACCGAGACA 422 Db 363 GGATGGACTTTTGGCTCAATATGGAGAACTGGAGAACAGTCAACACACAC

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APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER FILE REFERENCE: 21012.4.45509
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
SOFTWARET FILING DATE: 2300-06-28
SOFTWARET FILING DATE: PARLEQUES OF WINDOWS Version 3.0
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Patent No. 6531315
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Ralos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
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Best Local Similarity 66.6%; Pred. No. 5.4e-186;
Matches 979; Conservative 0; Mismatches 484;
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US-09-542-615A-175
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GENERAL INCORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Kalos, Michael D.
APPLICANT: Ranger, Chaitanya S.
APPLICANT: Banger, Chaitanya S.
APPLICANT: Fanger, Chaitanya S.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REPERBRUE: 210121.455268
CURRENT APPLICANT: NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 175
LENGTH: 4181
                                                                                                                                                1920 IGACTCAGGTAAAGCAGCACCAACAACAG 1948
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| Patent No. 6482597
| GENERAL INFORMATION:
| APPLICANT: Wang, Tongtong
| APPLICANT: Wang, Tongtong
| APPLICANT: Falos, Michael D.
| APPLICANT: Kalos, Michael D.
| APPLICANT: Falos, Michael D.
| APPLICANT: Falos, Michael D.
| APPLICANT: Alosen, Michael D.
| APPLICANT: Alosen, Michael D.
| APPLICANT: Alosen, Michael D.
| TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
| TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
| FILE REFERENCE: 210121.455C6
| CURRENT APPLICATION NUMBER: US/09/480,884A
| CURRENT APPLICATION NUMBER: US/09/480,884A
| SOFTWARE: FastSEQ for Windows Version 3.0
| SEQ ID NO 175
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Pred. No. 5.4e-186;
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Best Local Similarity 66.6'
Matches 979; Conservative
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NAME/KEY: misc feature
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ORGANISM: Homo sapiens
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       APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSEQ for Windows Version 3.0
ENGTH: 4181
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Best Local Similarity 66.6%; Pred. No. 5.4e-186;
Matches 979; Conservative 0; Mismatches 484;
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OTHER INFORMATION:
NAME/KEY: unsure
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OTHER INFORMATION:
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OTHER INFORMATION:
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26.09-643-597-175
; Sequence 155, Application US/09643597
; Patent No. 6426072
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Bangur, Chaitanya S
Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
Wang, Aijun
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Fan, Liqun
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APPLICANT: Wang, Tor
APPLICANT: Rangur, Ind
APPLICANT: Bangur, G
APPLICANT: Hosken, APPLICANT: Fanger, APPLICANT: Li, Samue
APPLICANT: Li, Samue
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**Sequence 4, Application US/09899651

* Sequence 4, Application US/09899651

* Patent No. 657676

* GENERAL INFORMATION:

* APPLICANT: Chen, Yao-Tseng

* APPLICANT: Chen, Yao-Tseng

* APPLICANT: Stockert, Elisabeth

* APPLICANT: Tsang, Solam

* APPLICANT: Stockert, Elisabeth

* APPLICANT: Gld, Lloyd J.

* APPLICANT: Old, Lloyd J.

* APPLICANT: Old, Lloyd J.

* APPLICANT: Associated Nucleic Acid Molecules Encoding Cancer

* APPLICANT: Associated Nucleic Acid Molecules Encoding Cancer

* TITLE OF INVENTION: Associated Nucleic Acid Molecules Encoding Cancer

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Pred. No. 5.4e-186;
0; Mismatches 484;
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ORGANISM: Homo
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                                CAGGTGCAGCTGAAAAAGCCATCAGTGCACTCCACCCCTGAGGGCTGCTCCTCCGCTT
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Sequence 4, Application US/09061709B

| Patent No. 6297364
| Patent No. 6297364
| GENERAL INFORMATION:
| APPLICANT: Chen, Yao-Tseng
| APPLICANT: Gure, Ali
| APPLICANT: Stockert, Elisabeth
| APPLICANT: Stockert, Elisabeth
| APPLICANT: Stockert, Elisabeth
| APPLICANT: Stockert, Elisabeth
| APPLICANT: Stockert, Elisabeth
| APPLICANT: Old, Lloyd J.
| TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated
| APPLICANT: Old, Lloyd J.
| TITLE OF INVENTION: Antigen, The Antigens Per Se, And Uses Thereof
| PILE REFERENCE: LUD 5538
| CURRENT APPLICATION NUMBER: US/09/061, 709B
| CURRENT FILING DATE: 1998-04-17
| NUMBER OF SEQ ID NOS: 8
| SEQ ID NO 4
| LENGTH: 4159
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                                                                                                           TGAAAATCATCGGACATTTCTATGCCAGTCAGATGGCTCAACGGAAGATCCGAGACATCC
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Pred. No. 5.4e-186;
0; Mismatches 484;
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Best Local Similarity 66.6%;
Matches 979; Conservative
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US-09-061-709-4
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US-09-061-709-4
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APPLICANT: Li, Samuel X.
APPLICANT: Li, Samuel X.
APPLICANT: Mang, Albun
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS ITTLE OF INVENTION: COMPOSITIONS OF LUNG CAIFER REFERENCE: 210121.455C9
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT PILING DATE: 2000-06-28
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 347.
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' Patent No. 6531315
' GENERAL INFORMATION:
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Bangur, Chaitanya
Hosken, Nancy
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APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael
APPLICANT: Bangur, Chaitan
APPLICANT: Hosken, Nancy
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-606-421B-347
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Best Local Similarity
Matches 980; Conserv
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TITLE OF INVENTION: COMPOUNDS AND METHODS ITITLE OF INVENTION: AND DIAGNOSIS OF LUNG CURRENT APPLICATION NUMBER: US/09/542,615A CURRENT APPLICATION NUMBER: US/09/542,615A SOFTWAREN FILING DATE: 2000-04-14 SUUMBER OF SEQ ID NOS: 350 SOFTWARE: PASKERQ FOR Windows Version 3.0
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APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy A.
APPLICANT: Fanger, Gary R.
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   APPLICANT: Henderson, Robert A.
APPLICANT: MCNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.45511
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FREISEQ for Windows Version 3.0
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Pred. No. 1.1e-186;
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66.78;
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Best Local Similarity 66.7
Matches 980; Conservative
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CRGANISM: Homo sapiens
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Best Local Similarity 83.5%; Pred. No. 0; Matches 1556; Conservative 0; Mismatches 275; Indels 33; 108 AGGAGCGGAAATTCAATTCGAATTTCACCCCAGCTCCGATGGGAAGTAC	rgaag agcag agcag	408 468 725		GCAAG TTCCC TTCCC	OY 708 CTGAAGATCCTGGCCATAATTACTAGGGGTCTCATTGGCAAGGAAGG		948 AGCTCTCACCTGATCCCTGGCTGCTGTAGGTCTTTTCCCAGCT 1001 1 1 1 1 1 1 1 1

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TTGCCAGCGCCTCCATCAAGATTGCACCACCGGAAACACCTGACTCCAAAGTTCGTATGG
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; Pred. No. 0;
0; Mismatches
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larity 99.8%;
Conservative
 PRIOR FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 5
                                                   TYPE: DNA ORGANISM: Homo sapiens
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Best Local Simi
Matches 1676;
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                                                                                 ; FEATURE:
US-09-899-651-5
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; Batent No. 6576756
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Tsang, Solam
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Knuth, Alexander
; APPLICANT: Knuth, Alexander
; APPLICANT: Chen, Solated
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer
; TITLE OF INVENTION: Associated
; TITLE OF INVENTION: Antigen, The Antigens Per Se, And Uses Thereof
; TITLE OF INVENTION: UNDEST: US/09/899,651
; CURRENT APPLICATION NUMBER: US/09/061,709
; PRIOR APPLICATION NUMBER: US/09/061,709
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Pred. No. 0;
0; Mismatches
CURRENT APPLICATION NUMBER: US/09/061,709B
CURRENT FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 5
LENGTH: 1708
                                                                                                                                       Query Match 85.8%;
Best Local Similarity 99.8%;
Matches 1676; Conservative
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                                                                   TYPE: DNA
ORGANISM: HOMO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes human lung tumour proteins. Human lung tumour proteins and polynucleotides have cytostatic and immunostimulant activities, and can be used in vaccine production. Compositions comprising the lung tumour proteins, polynucleotides, antibodies, fusion proteins, T cell populations, or antigen presenting cells that express the lung tumour proteins are useful for treating lung cancer or stimulating an immune response. ABLA8959 to ABLA9300 and ABB74946 to ABB75070 represent sequences used in the exemplification of the present
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, Peckham DW;
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                                                                                                                                                                                                            The present invention describes human lung turmour proteins. Human lung turmour proteins and polynucleotides have cytostatic and immunostimulant activities, and can be used in vaccine production. Compositions comprising the lung turmour proteins, polynucleotides, antibodies, fusion proteins, T cell populations, or antigen presenting cells that express the lung turmour proteins are useful for treating lung cancer or stimulating an immune response. ABL48959 to ABL49300 and ABR74946 to ABB75070 represent sequences used in the exemplification of the present
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0; Mismatches 483; Indels 6;
          GR;
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            Fanger
                                                                                                                  Polynucleotides encoding lung tumor polypeptides, lung cancer or stimulating an immune response.
      Marnerakis M,
Peckham DW;
      Retter MW,
Watanabe Y,
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                predetermined cut-off value, and determining the presence of a cancer in the patient. (1) and (11) are useful in pharmaceutical compositions, e.g. vaccines. (1) is useful as a marker to indicate the presence or absence of a cancer such as lung cancer. ABQ92145 to ABQ92486 and ABP61866 to ABP61992 represent sequences used in the exemplification of the present
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Pred. No. 4.6e-177;
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	223 GTGAGACGGCAGTGGTGAATGTCACCTATTCCAACCGGGAGCAGCCAGGCAAGCCATCA 282 	283	343 AGCAGATAGCACAGGACCTGAGAATGGGCGCCGAGGGGCTTTGGCTCTCGGGGTCAGC	46 58	GGGGCCA 52 GGTGCCA 64	523 CCÀTCGGCAACATCACAAAACAGACCCAGTCCAAGATAGACGTGCATAGGAGAGGAGAACG 582 	583 CAGGIGCAGCIGAAAAAGCCAICAGIGTGCACCCCIGAGGGCIGCICCCCCCGCII 642 	643 GTAAGAIGAICTIGGAGAITAIGCAIAAAAGGGCTAAGGACACCAAAACGGCIGACGAGG 702 				883 GCAGGGCCGAGAAATAATGAAGAAGATCAGGAGCCTATGAGAATGATGATGGCGG 942			GCTCCTTTATGCAGGCTCCCGAGCAGAGATGGTGCAGGTGTTTATCCCGGCCCAGGGGGAGATGGTGCAGGTGTTTATCCCGGCCCAGGGAGATGGTGCAGGTGCTTATCCCCGCCCAGGGAGGTGCAGGAGATGGTGCAGGTGTTTATCCCCGCCCAGGCAGG	TGGGCGCCATCATCGCAAAAAAGGGCAGCACATCAAAAGGCTCCCGGTTTGCCAGCG		AGGAGG
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ACCAGAGGCTCAGTTCAAGGCTCAGGGAAGAATTTATGGAAAAATTAAAGAAG 1429
                                                                           IGITAGTCCTAAAGAAGAGGTGAAACTTGAAGCTCATATCAGAGTGCCATCCT 1489
                                                                                                                             TGGCCGGGTCATTGGCAAAGGTGGAAAAACGGTGAACGAGTTGCAGAATTTGA 1416
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                                         CTITGGTCCCAAGGAGGAAGTGAAGCTGGAGACCCACATACGTGTGCCAGCAT
                                                                                                                                                                                                                                                          CATCGGACATTICTATGCCAGTCAGATGGCTCAACGGAAGATCCGAGACATCC
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jer N, Retter MW, Durham M, Fanger GR, Vedvick TS;
ibe Y, Peckham DW, Cai F, Foy TM;
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TGGACAGCCTGCTGGCTACAGTACGGTACAGTAGAACTGTGAGCAAGTGAACACCGAGA 222
TGAAAATCATCGGACATTTCTATGCCAGTCAGATGGCTCAAACGAAGATCCGAGACATCC 1536
                                                                        TGGCCCAGGTTAAGCAGCAGCATCAGAAG
                                                                                            Example 2; Page 330; 374pp; English.
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rcaaaaraacrigiriciriririciriscedagirgeeeagaaaaarreagaaarre 1669
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PD, Fanger N, Retter MW, Marnerakis M,
TS, Carter D, Watanabe Y, Peckham DW;
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Pred. No. 4.6e-177;
0; Mismatches 483;
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treatment; human; tumor; immunogenic; cytostatic;

cancer; therapy;

990S-00285479. 990S-00466396. 990S-00476496. 2000US-00480884.

CORIXA CORP

Fan L;

2000WO-US008896

cDNA antigen L523S

(first entry)

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This invention describes a novel isolated polypeptide (I) which which which have cytostatic activity. The polypeptides and polynuclectides are used in compositions and vaccines to inhibit the development of cancer, especially lung cancer, in a patient. Methods described in the invention detection at subsequent time points and comparing the results from the different time points and comparing the results from the different time points. CD4+ and/or CD8+ T-Cells isolated from a patient are treated with P2, polynucleotides encoding P2 or antigen presenting cells expressing P2 and then administered to the patient to inhibit
                                                                                                                                                                                                                                                                                                                                                    Isolated polypeptide comprising an immunogenic portion of a lung protein is used for detecting and monitoring progression of lung in a patient.
                                                                                                                                                                                                                                                                                                                                                                                                Claim 1a; Page 258-259; 261pp; English.
                                                    Human lung cancer-associated
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                                                                                     vaccine; detection;
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30-DEC-1999;
10-JAN-2000;
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methods. The present sequence was used as the representative sequence from a human clone which was used in homology searches to identify the clone. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from
                                                                                                                                                     GAGATTATGCATAAAGAGGCTAAGGACACCAAAACGGCTGACGAGGGTTCCCCTGAAGATC
                                                                                                                                                                                                                                                                          AAAGCCATCAGTGTGCACTCCACCCCTGAGGGCTGCTCCTCCGCTTGTAAGATGATCTTG
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                                                                                              Length 833;
                                                                     C; 215 G; 166 T; 0 U; 4 Other;
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                                                                                                                  14; Indels
                                                                                             DB 4;
                                                                                        37.7%; Score 732.8; DB 4; llarity 96.9%; Pred. No. 1.5e-193; Conservative 0; Mismatches 14;
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                                                                                                        Gaps
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                                                Score 674.2; DB 3; Length 1740;
Pred. No. 4.6e-177;
0; Mismatches 483; Indels 6;
Sequence 1740 BP; 526 A; 406 C; 417 G; 391 T; 0 U; 0 Other;
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al Similarity 66.7%;
980; Conservative 0
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BP.

standard; cDNA; 1740

AAC66035

RESULT 11
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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special
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T, Koga
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S, Otsuki
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K, Kojima
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a T, Nagai I
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11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183765.
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K, Kojima S, Otsuki T, Koga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 833 BP; 223 A; 225 C; 215 G; 166 T; 0 U; 4 Other;
                     Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
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Pred. No. 1.5e-193;
0; Mismatches 14;
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Wakamatsu A, Sugiyama T, Nagai
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2000JP-00118774.
2000JP-00183765.
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Matches 802; Conservative
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                                                                        Homo sapiens
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AGCAGCGTTACTGGGGCTGCTCCCTATAGCTCCTTTATGCAGGCTCCCCGAGCAGAGATG 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGAACCTGGCTGTAGGTCTTTTCCCAGCTTCATCCAGGGCAGTCCCGCCGCCTCCC 1028
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e, gastrointestinal, pulmonary, cardiovascular or
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Pred. No. 2e-287;
3; Mismatches 5; Indels
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27-SEP-2000; 2000US-0235834P.
29-SEP-2000; 2000US-0236327P.
29-SEP-2000; 2000US-0236367P.
29-SEP-2000; 2000US-0236368P.
29-SEP-2000; 2000US-0236368P.
29-SEP-2000; 2000US-0236369P.
02-OCT-2000; 2000US-0236370P.
02-OCT-2000; 2000US-0237038P.
02-OCT-2000; 2000US-0237038P.
02-OCT-2000; 2000US-0237038P.
13-OCT-2000; 2000US-0237040P.
13-OCT-2000; 2000US-02340960P.
20-OCT-2000; 2000US-024188P.
20-OCT-2000; 2000US-024188P.
21-NOV-2000; 2000US-024180P.
01-NOV-2000; 2000US-024180P.
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inhibiting or preventing e.
respiratory, reproductive,
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TTCCAGTGAGGAACCCTGATCTNTCAGCCCCCAACCCCACCCAATTGGCCCCAACACTGT
                                                                                     1809 NIGCCCCICGGGGIGICAGAAATINIAGCGCAAGGCACTITIAAACGIGGALIGITTAAA
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                                 Human novel polynucleotide #735.
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2000US-0220963P.
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2000US-0234997P.
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14-AUG-2000; 2
14-AUG-2000; 22-AUG-2000; 32-AUG-2000; 31-AUG-2000; 31-AUG-2000; 01-SEP-2000; 0
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05-SEP-2000;
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                    to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be use as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present sequence encodes a novel secreted protein of the invention. Note: The sequence data for this patent did not form part of the printed
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Ruben SM; Rosen CA, Barash SC,

WPI; 2001-488783/53. P-PSDB; AAU16579.

New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives.

Claim 1; SEQ ID NO 745; 980pp; English.

The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic confined symptoms associated with the disorders and in diagnostic confined in alleviating symptoms associated with the disorders and in diagnostic confined in a line of the protein confined in the disorders and in diagnostic constant in the sease e.g. rheumatoid arthritis, hyperproliferative disorders e.g. corplasms of the breast or liver, cardiovascular disorders e.g. cardior concepts of the confined confi

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Human; immunosuppressive; antiarthritic; ss; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; Myperpoliferative disorder; cardiac arrest; cerebrovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; skin ageing; food additive;
CTGTCCCTINGAGTCCAGGACAACAACGGGCAGAAATCGAGAGTGTGCTCTCCCCGGCAG 1672
                                                                                                            ATTGGCCCAACACTGTNTGCCCCTCGGGGTGTCAGAAATTNTAGCGCAAGGCACTTTTAA
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                                                                             Human cDNA encoding a novel secreted protein, Seq ID 745.
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                 polynucleotides. The polypeptides and polynucleotides are useful in gene therapy for treating, inhibiting or preventing neural disorders, immune system disorders (e.g. systemic lupus erythematosus, rheumatoid arthritis and multiple sclerosis), muscular disorders, respiratory diseases (e.g. nasal vestibulitis, nasal polyps and sinusitis), reproductive disorders, gastrointestinal disorders, pulmonary disorders, cardiovascular disorders (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left heart syndrome), renal disorders (e.g. acute kidney failure and end-stage renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and leukaemia), inflammatory diseases (e.g. septic shock, bursitis and appendicitis), allergic reactions and conformation and cancertous diseases. Sequences ABX71173-ABX74167 represent human novel polynucleotides of the invention
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             The polypeptides and polynucleotides are useful in gene
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17-JAN-2001; 2001US-00764864

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11.-UUL.-2000; 21.-UUL.-2000; 22.-UUL.-2000; 22.-UUL.-2000; 22.-UUL.-2000; 22.-UUL.-2000; 23.-UUL.-2000; 23.-UU

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Human; gene; ds; neural disorder; immune system disorder; renal disorder; muscullar disorder; respiratory disease; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; hyperproliferative disorder; inflammatory disease; allergic reaction; blod related disorder; cancer; immunosuppressive; antinflammatory; cardiovascular; nephrotropic; cytostatic; antiallergic; thrombolytic; haemostatic; antiarterioscherotic.
                      ΒP
                                                                                                                  Human novel polynucleotide #317.
                 ABX73489 standard; DNA; 1182
                                                                                   (first entry)
                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                               18-MAR-2003
                                                   ABX73489
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New polypeptides and nucleic acids, useful in gene therapy for treating, inhibiting or preventing e.g. neural, immune system, muscular, respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or renal disorders. WPI; 2003-147444/14. P-PSDB; ABU55229.

Barash SC;

Rosen CA, Ruben SM,

2000US-0240960P. 2000US-0241785P. 2000US-0241809P.

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29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 20-CT-2000; 2

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08-DEC-2000;

ROSEN C A. RUBEN S M. BARASH S

(ROSE/) (BARA/) Claim 1; SEQ ID NO 327; 402pp; English.

The invention relates to human novel polypeptides and their associated

US2002132753-A1

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2000US-0241808P.
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AATAATGAAGAAAGTTCGGGAGGCCTATGAGAATGATGTGGGCTGCCATGAGC-----TC

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1193 ACCACCGGAAACACCTGACTCCAAAGTTCGTATGGTTATCATCACTGGACCGCCAGAGGC 1252

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The invention relates to isolated nucleic acid molecules and their cencoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, crabbits goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a completion. Antibodies to the proteins can also be used in pathological condition. Antibodies to the proteins can also be used in assays immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays immunoassays e.g. redioimmunoassays or enzyme linked immunosorbant assays (BLISA). Disorders which are diagnosed or treated include autoimmune (Grasases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. arrest, cerebrovascular disorders e.g. cerebral ischaemis, angiogenesis, arrest, cerebrovascular disorders e.g. cerebral ischaemis, angiogenesis, carest, orenebral dungi and ocular disorders e.g. corneal infection, and many other disorders e.g. Alzheimer's disorders e.g. corneal infection, and many other disorders e.g. Alzheimer's disorders e.g. corneal infection, corner also be used to aid wound healing and epithelial cell proliferation, corpresent skin aging due to subburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutrititional components. The present sequence encodes a novel secreted protein of the present ceregement of the printed for sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                       New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1085.4; DB 4; Length 1182;
Pred. No. 9.1e-292;
0; Mismatches 6; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 327; 980pp; English.
                                                                                                                                                                                                       Barash SC, Ruben SM;
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08-DEC-2000; 2000US-0251869P.
08-DEC-2000; 2000US-025199PP.
11-DEC-2000; 2000US-025199PP.
05-JAN-2001; 2001US-0259678P.
                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC
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Best Local Similarity 98.9
Matches 1102; Conservative
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P-PSDB; AAU16161.
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secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; skin ageing; food additive; preservative; antiproliferative.
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2000US-018062BP.
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2000US-0189774P.
2000US-0199076P.
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17-MAR-2000;
18-APR-2000;
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            CCGCCAGAGGCCCAATTCAAGGCTCAGGGAAGAATCTATGGCAAACTCAAGGAGAAC 1301
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                                                                 ATCAAGATTGCTCCACCAGAAACACCTGACTCCAAAGTTCGAATGGTCGTCATCACTGGA
                                        ATCAAGATTGCACCACCCGAAACACCTGACTCCAAAGTTCGTATGGTTATCATCACTGGA
                                                                                                                                                                          Tritidericicaaggaggagraaagcragaggcccacaraccaggrrcggcrrcagca
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                                                                                                                                                                                                                                           cDNA encoding a murine c-myc coding region determinant binding protein.
                                                                                                                                                                                                                                                            c-myc;
                                                       CCCTGTCCCTTCGAGTCCAGGACAACAACGGGCAGAAATCGAGAGTGTGTCTCCCCGGGC
                                             ACTIGATICAGAAAGAIGTICCAGTGAGGAACCCTGAICTNICAGCCCCAAACACCCCACC
                                                                                       CAATTGGCCCAACACTGTNTGCCCCTCGGGGTGTCAGAAATTNTAGCGCAAGGCACTTTT
                AGGCCTGAGAATGAGTGGGAATCCGGGACACNTGGGCCGGGCTGTAGATCAGGTTTGCCC
                                                                                                                                                                                                                                                            tumor;
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The present sequence encodes a murine c-myc coding region determinant binding protein (CRD-BP). The presence or absence of a tumor can be determined by determining the levels of CRD-BP present in the suspect tissue, where the CRD-BP shields c-myc RNA from endonucleolytic attack and so prolongs its half-life. The methods are used for diagnosing presence or absence of a tumor in a human, especially breast, colon and pancreatic cancer. They are also used to inhibit cancer cell growth

BP; 580 A; 609 C; 618 G; 417 T; 0 U; 0 Other;

Sequence 2224

C-myC

Diagnosing presence or absence of a tumor in a human by examining coding region determinant-binding protein.

79pp; English.

1A-D;

Example; Fig

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                                                                  AGGAGCCGGAAAATTCAAAATCCCGAACCCCCCAGCTCCCGATGGGAAGTACTGGAC
                                                                                                  AGGAGTCGGAAAATACAGATCCGCAATATTCCACCTCAGCTCCGATGGGAAGTGCTAGAT
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Score 1297.8; pred. No. 0; 0; Mismatches
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                                            CAAGAGGGTGGATCACACCTCAGTGGGAAGAAAATAAATTTCCTTCAGGTTTTAAAA 1946
                                                                   Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
                                                                                                                                  Human full-length cDNA, SEQ ID NO: 3886.
                                                                                                 AAK94782 standard; cDNA; 2780 BP
                                                                                                                                                                                          07-JUL-2000; 2000EP-00114089.
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Kawai Y; T, Koga Hayashi K, Ishii S, K, Kojima S, Otsuki Isogai T, a T, Nagai Wakamatsu A, Sugiyama T, Nishikawa T, Ė

(HELI-) HELIX RES INST

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2001-524255/58. P-PSDB; AAM93826

) Primers useful for synthesizing full length cDNA clones and their use genetic manipulation. 830 Primers useful

Claim 8; SEQ ID NO 3886; 1380pp + Sequence Listing; English.

The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nuclectide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers mable the production of the full length cDNA assily without any special methods. The present sequence is a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly

Sequence 2780 BP; 768 A; 681 C; 671 G; 660 T; 0 U; 0 Other;

6; Gaps 71.4%; Score 1389; DB 4; Length 2780; llarity 99.2%; Pred. No. 0; Conservative 0; Mismatches 5; Indels 6 Indels 5; Query Match Best Local Similarity Matches 1405; Conserv

537 ACAAAACAGACCCAGTCCAAGAIAGACGIGCAIAGGAAGGAGAACGCAGGIGCAGCIGAA 596

1;

 1 ACAAAAC	OY 597 AAAGCCATCAGGGACCCCGGAGGGCTGCTCCTCGCCTTGTAAGATGATCTTG	OY 657 GAGATTATGCATAAAGAGGCTAAGGACACCAAAACGGCTGACGAGGTTCCCCTGAAGATW	OY 717 CTGGCCCATAALTAGTAGGGGTCTCATTGGCAAGGAAGGACGGAACCTGAAGAAG 	777 GTAGAGCAAGATACCGAGACAAAAACC 	837 AACCTGAGAGGACCATCACTGTGAAGGGGGCCATCGAGAATTGTTGCAGGGCCGACA.	897 GAAATAATGAAGAAGCCTATGAGAATGATGGCCCATGCGAGGACCCATGCGAGCCCAGGCCCAACCAA	951 TCTCACCTGACCTGACCTGACCTATCAGAATGATGATGTGCGCTGCCATGAGCCTGCA	421 TCTCA	1011 GCAGTCCCGCGCCTCCCAGCAGCGTTACTGGGGCTGCTCCCTATAGCTCCTTTATGCAG	1071 GCTCCCGAGCAGGAG 	1131 GGCAAGAAGGGGCAGCACCAACCAAGCTCTCCCGGGTTTGCCAGCGCCTCCATCAAGATTA	1191 GCACCACCGGAAACACCTGACTCCAAAGTTCGTATGGTTATCATCACGGACC 	1251 GCCCAATTCAAGGCTCAGGGAAGAATCTATGGCAAACTCAAGGAGGAGAACTTTT 	1311 CCCAAGGAAGTGAAGCTGGAGACCCACATACGTGTGCCAGCATCAGCAGCTGGC	1371 GTCATTGGCAAAGGTGGAAAAACGT 	1431 GTAGTACCAAGACCAGACCCCTGATGAGAACGACCAGGTCATGGTGAAAA 	1491 CATITCTATGCCAGTCAGGGGGAGGAGGTCCGAGACATCCTGGCCCAGGTT	aagtgac aagtgac	1611 CCCTGTCCCTTNGAGTCCAGGACAACAACGAGAAATCGAGAGTGTGCTCTCCCGGC
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The present sequence represents a cancer associated antigen gene designated KOC-2. The specification also describes a cancer associated antigen designated CT7. The CT7 polynucleotide was isolated from SK-MEI-CC antigen designated CT7. The polypeptide has some homology with MAGE-10, implied to about 210 carboxy terminal amino acids. The amino terminal of the protein has a repetitive pattern, with repeats rich in serine, the protein has a repetitive pattern, with repeats rich in serine, proline, glutamine and leucine, and an almost invariable core of the peptides which provoke lysis by cytolytic T cells. The polynucleotides and polypeptides can be used for treating a cancerous condition and antigens can be used as an immunogenic or vaccine composition with an antigens can be used as an immunogenic or vaccine composition with an adjuvant, e.g. a cytokine, a saponin, or granulocyte macrophage-colony contains the cancer (GM-CSF)
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An alternative form of DNA encoding cancer associated antigen KOC-2. Cancer associated antigen; KOC-2; cancer; vaccine; CT7; ss. AAZ36153 standard; DNA; 1946 BP. (LUDW-) LUDWIG INST CANCER RES. 98US-00061709. 99WO-US005766. (first entry) Homo sapiens. WO9954738-Al 16-MAR-1999; 11-FEB-2000 17-APR-1998; 28-OCT-1999. AAZ36153; AAZ36153

Knuth A, Stockert E, Jager E, ທ່ Tsang WPI; 2000-013284/01. Gure A, Chen Y,

old LJ;

Nucleotides representing cancer-associated genes, used to develop products for the diagnosis, monitoring and treatment of cancers.

Claim 55; Page 42; 44pp; English.

The present sequence represents an alternative form of a cancer associated antigen gene designated KOC-2. The specification also describes a cancer associated antigen designated CT7. The CT7 polypucleotide was isolated from SK-MEL-37 melanoma cells. The polypeptide has some homology with MAGE-10, limited to about 210 carboxy terminal amino acids. The amino terminal of the protein has a repetitive pattern, with repeats rich in serine, proline, glutamine and leucine, and an almost invariable core of the peptide given in AAV43877. The CT7 polypeptide can be processed to peptides which provoke lysis by cytolytic T cells. The polymucleotides and polypeptides can be used for treating a cancerous condition and screening for or diagnosing cancerous conditions. The cancer associated antigens can be used as an immunogenic or vaccine composition with an adjuvant, e.g. a cytokine, a saponin, or granulocyte

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	ctgaagatcctggcccataataactttgtagggggtctcattggcaaggaagg	CTGAAGAAGGTAGAGGAAGATACGGAGACAAAATCACCATCTCCTGGTTGCAAGACCTTTGAAGAAAGA	acctitacaacctgaggaccatcactgtgaaggggccatcgagaattgttgcagg 	CCGAGCAGGAAATAATGAAGAAAGTTCGGGAGGCCTATGAGAATGATGTGGCTGCCATG 	AGCTCTCACCTGATCCCTGGCCTGAACCTGGCTGTAGGTCTTTTCCCAGCT	TCATCCAGCGCAGTCCCGCCGCCAGCGTTACTGGGGCTGCTCCTATAGCTCC	TTATGCAGGCTCCCCAAGCAGAAGATGGTGCAGGTGTTTATCCCCGCCCAGGCAGTGGCCCCAGCAGTGGCCAGCAGAGACGTACACGTTCATCCTCCTGCCCAAGCGGTTGGT	GCCATCATCGGCAAGAAGGGGCAGCACTCAACAACAGCTCTCCCGGTTTGCCAGCGCCTCC	atcaagattgcaccaccggaaacacctgactccaaagtrcgtatggttatcatcactgga 	ccgccagaggcccaattcaaggctcagggaagaatctatggcaaactcaaggaggagaac 	TTCTTTGGTCCCAAGGAAGTGAAGCTGGAGACCCACATACGTGTGCCAGCATCAGCA 	GCTGGCCGGGTCATTGGCAAAGGTGGAAAAACGGTGAACGAGTTGCAGAATTTGACGGCA 	gctgaggtggtagtaccaagagcccagacccctgatgagaacgaccaggtcatcgtgaaa 	atcatcggacatitictatgccagtcagatggctcaacggaagatccgagacatccfgcc 	CAGGTTAAGCAGCACCACCAGGGACAGAGTAACCAGGCCCAGGCAGG
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ANVITGPPEAQFKAQGRIYGKLKEENFFGPKEEVKLETHIRVPASAAGRVIGKGKT
NNELQNLTAAEVVVVPRDQTPDENEQVIVKIIGHFYASQMAQRKIRDILAQVKQQHQKG
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1620. .1646
/gene="ZBP1"
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/gene="ZBP1"
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NTKKQTQSKIDVHRKENAGAAEKAISHSTPBGCGAACKMILEIMQKEAKDTKTADE
VPLKILAHNNFYGRLIGKEGRNLKKVEQDTETKTISSLQDITLYNPBRITTVKGSIE
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AAPYSSFMPPEQETVHVFIPAQAVGAIIGKKCQHIKQLSRFASASIKIAPPPFPDSKV
                                                                             ATCATCGGACATTTCTATGCCAGCCAGATGGCCCAGCGGAAGATCCGAGACATCCTGGCT 1896
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PDEQWAMKAIETFSGKVELHGKQLEIEHSVPKKQRSRKIQIRNIPPQLRWEVLDGLLA
QYGTVENCEQVNTDSETAVVNVTYTNREQTRQAIMKLNGHQLENHVLKVSYIPDEQSV
1777 GCCGAGGTGGTCGTGCCGAGAGACCAGACCCAGACGAGAACGACCAAGTCATTGTTAAG 1836
                                       ATCATCGGACATTTCTATGCCAGTCAGATGGCTCAACGGAAGATCCGAGACATCCTGGCC 1541
                                                                                                                     CAGGITAAGCAGCATCAGAAGGGACAGAGTAACCAGGCCCAGGCACGGAGGAAGTGA 1601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus
Mararyota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae,
Phasianinae, Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Einstein College of 10461, USA
                                                                                                                                                                                                                                         /function="binds a zipcode element in beta-actin mRNA 3/UTR and is involved in its localization" /note="beta-actin mRNA zipcode-binding protein"
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Ross, A.F., Oleynikov, Y., Kislauskis, E.H., Taneja, K.L. and
Singer, R.H.
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Gallus gallus zipcode-binding protein (ZBP1) mRNA,
AF026527
                                                                                                                                                                                                   -CCAGCCCTCCCTGTCCCTTNGAGTCCAGGACAACAACGGGCAGA-
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Oleynikov,Y.S., Ross,A.F. and Singer,R.H.
Direct Submission
Direct (24-SEP-1997) Cell Biology, Albert
Medicine, 1300 Morris Park Avenue, Bronx, NY
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/product== zipcode-binding protein"
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/db_xref==GI:S270921"
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/db_xref="taxon:9031"
/cell_type="fibroblast"
/dev_stage="embryo"
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ATAGCACAAGGTCCTGAGAATGGGCGCGTGGAGGCTTTGGGTCTCGAGGCCAGGCCCAGG
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                                                        CAGGGCTCACCTGTGGCAGCGGGCCCCCAGCCAGCAGCAGCAGTGGACATCCCCCTT
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VPLKILAHNNEVĞRI IĞKEĞRNIKKVYEĞDTETKI TI SSLQDILTLINEBRITIVKĞALE
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QYGTVENCEQVNTESETAVVNVTYSNREQTRQAIMKLNGHQLENHALKVSYIPDEQIA
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Eom,T., Singer,R.H. and Bassell,G.J.

Direct Submission

Submitted Und-2002) Neuroscience, Albert Einstein College of
Medicine, 1300 Morris Park Ave., Bronx, NY 10461, USA

Location/Qualifiers
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Localization of a beta-actin messenger ribonucleoprotein complex
with zipcode-binding protein modulates the density of dendritic
filopodia and filopodial synapses
J. Neurosci. 23 (32), 10433-10444 (2003)
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Villalon, D. K., Muzny, D. M., Sodergren, E. J., Lu, X., Gibbs, R. A., Pahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Buffard, G.G., Blakeley, R. W., Touchman, J. W., Green, E. D., Dickson, M. C., Rodriguez, A. C., Grimwood, J., Schmutz, J., Myers, R.M., Shuterfield, Y. S., Krzywinski, M. I., Skalska, U., Smailus, D. B., Schnerch, A., Schein, J. E., Jones, S. J. and Marra, M. A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S. A. 99 (26), 16899-16903 (2002)
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Submitted (30-APA-2003) National Institutes of Health, Mammalian
Submitted (30-APA-2003) Cancer Genomics Office, National Cancer
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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web site: http://www.hgsc.bcm.tmc.edu/cdna/
Web site: http://www.hgsc.bcm.tmc.edu
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.
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Tissue Procurement: Dr. Kenneth R. Boheler (National Insitute
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/db xxef="MGI:1890357"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Mus musculus insulin-like growth factor 2, binding protein 1, mRNA (CDNA_Clone MGC:60613 IMAGE:30008106), complete cds.
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AAPYSSFMOAPEQENVQVFIPAQAVGAIIGKKGQHIKQLSRFASASIKLAPPETPDSK
VRMVJITGPPEAQFKAQGRIYGKLKEENFFGPKEEVKLETHIRVPASAAGRYIGKGGK
TVNELQNLTAAEVVVPRDQTPDENDQVIVKIIGHFYASQMAQRKIRDILAQVKQQHQK
GQSNLAQARRK"
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QYGTVENCEGPGSRGQPRQASPVAAGAPAKQQPUDIALLLYPTQYYAAIIGKEGATI
RNITKQTQSK LDVHRENAGABRAIS SUHSTPEGCSBACKMILEIMHKEAKDFTATADE
VPLKILAHNNFVGRLIGKEGRNLKKVEQDTETKITISSLQDLTLYNPERTITVKGAIE
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PDEHWAMKAIETFSGKVELQGKRLEIEHSVPKKQRSRKIQIRNIPPQLRWEYLDSLLA
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                                                                                                                                                                                                                4 (bases 1 to 2223)
Leeds P., Kren, B.T., Boylan, J.M., Betz, N.A., Steer, C.J.,
Gruppuso, P.A. and Ross, J.
Developmental regulation of CRD-BP, an RNA-binding protein that
stabilizes c-myc mRNA in vitro
Oncogene 14 (11), 1279-1286 (1997)
                                                                                                                                                                                                                                                                                                                                  5 (bases 1 to 2223)
Doyle,G.A., Betz,N.A., Leeds,P.F., Fleisig,A.J., Prokipcak,R.D.
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                                                                                                                                                                                                                                                                                                                                                                               protein: a member
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/protein id="AAC72743.1"
/db_xref="GI:3273749"
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Pred. No. 7.4e-308;
0; Mismatches 269; Indels 34;
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Submitted (25-APR-1998) McArdle Laboratory, University of Madison, 1400 University Ave., Madison, WI 53706, USA Location/Qualifiers
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                                                                                                              3 (bases 1 to 2223)
Probipcak, R.D., Herrick, D.J. and Ross, J.
Purification and properties of a protein that I C-terminal coding region of human c-myc mRNA 94179348
                                                                                                                                                                                                                                                                                                                                                                           The c-myc coding region determinant-binding family of KH domain RNA-binding proteins Nucleic Acids Res. 26 (22), 5036-5044 (1998)
                                                                     Mol. Cell. Biol. 14 (3), 2119-2128 (1994) 94158886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. 2223
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
2 (bases 1 to 2223)
Herrick, D.G. and Ross, J.
The half-life of c-myc mRNA in influence of the coding and 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
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                              ACAGGGGGGGTCAACGTACTCTAACCGGGAGCAGACCAGGCAAGCTATCATGAAG
                                                                                                       CTGAATGGCCACCAGTTGGAGAACCATGCCCTGAAGGTCTCCTACATCCCCGATGAGCAG
                                                                                                                                   545 CTAAATGGCCATCAACTGGAGAGAACCTGAAGGTCTCCTACATACCTGATGAGGAG
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c-myc coding region determinant-binding protein (CRD-BP) and its nucleic acid sequence
Patent: US 6255055-A 1 03-JUL-2001;
                CCCAAGGAGGAAGTGAAGCTGGAGACCCACATACGTGTGCCAGCATCAGCAGCTGGCCGG
                                   781 CCCAAGGAGGAAGTGAAGTTGGAGACCCACATACGTGTGCCAGCATCAGCAGCTGGCGG
                                                                                                           841 GTCATTGGCAAAAGGTGGAAAAACGGTGAACGAGTTGCAGAATTTGACGGCAGCTGAGGTG
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                                                                                                                                                                                                                              1141 AGGCCTGAGAATGAGTGGGAATCCGGGACACCTGGGCCGGGCTGTAGATCAGGTTTGCCC
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                                                                                                                                               GTAGTACCAAGAGACCAGACCCCTGATGAGAACGACCAGGTCATCGTGAAAATCATCGGA
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Best Local Similarity 83.5%; Pred. No. 1.9e-308;
Matches 1556; Conservative 0; Mismatches 275;
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/wol_type="unassigned DNA"
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Sequence 1 from patent US 6255055.
AR160244 GI:16223887
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Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass Sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.).

Location/Qualifiers

1. .2780

/organism="Homo sapiens"
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/clone_lib="NT2RP3"
/note=loning vector: pMEB8FL3-mRNA from NT2 n
precursor cells after 2-weeks retinoic acid (RA)
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cive 0; Mismatches
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/db_xref="taxon:9606"
/clone="NT2RP3000789"
/cell_line="NT2"
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Homo sapiens cDNA FLJ90434 fis, clone NT2RP3000789, highly similar to Homo sapiens IGF-II mRNA-binding protein 1 (IMP-1) mRNA.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                        C C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00
Primer for synthesizing full-length cDNA and use thereof FH K
Location/Qualifiers
 GCCCAATTCAAGGCTCAGGGAAGAATCTATGGCAAACTCAAGGAGGAGGAGAACTTCTTTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAAGCCATCAGTGTGCACTCCACCCCTGAGGCTGCTCCTCCGCTTGTAAGATGATCTTG
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Location/Qualifiers
                                                                                                                                                                                                                                                                              Score 1389;
Pred. No. 0;
                                                                                                                                                                    1. .2780/
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                            71.4%;
ilarity 99.2%;
Conservative
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07-JUL-2000 JP 2000253172
TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
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YURI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI, PI
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Primer for synthesizing full-length cDNA and use thereof
Primer for synthesizing full-length cDNA and use thereof
Patent: UP 2002017375-A 3242 22-JAN-2002;
PR JOSHAN-2002
PF 07-JUL-2000 JP 200253172
PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, S
PI SHII,
PI YURI KAWAI,AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NACAI SHINCHI KOJIMA,
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JP 2002017375-A/3242.

Homo sapiens (human)

Homo sapiens
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LOCUS
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AUTHORS
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 /db_xref="taxon:9606"
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Chen.Y.-T., Gure.A., Tsang.S., Stockert,E., Jager,E., Alexander,K.
Chen.Y.-T., Gure.A., Tsang.S., Stockert,E., Jager,E., Alexander,K.
and Old,L.J.
Isolated nucleic acid molecule encoding cancer associated antigen,
the antigen itself, and uses thereof
Patent: US 6297364-A 5 02-OCT-2001;
Location/Qualifiers
1. .1708
/mol_type="unknown"
/mol_type="unassigned DNA"
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                      TTCTTTGGTCCCAAGGAGGAAGTGAAGCTGGAGACCCACATACGTGTGCCAGCATCAGCA
                                                                  CCAGCCCCTCCCTGTCCCTTNGAGTCCAGGACAACAACGGGCAGAAATCGAGAGTGTGCT
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                                                     GCTGGCCGGGTCATTGGCAAAAGGTGGAAAAACGGTGAACGAGTTGCCAGAATTTGACGGCA
                                                                                                   GCTGAGGTGGTACCAAGAGACCAGACCCCTGATGAGAACGACCAGGTCATCGTGAAA
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NVTYSNREQTRQAIMKLNGHQLEHALKVSYTPDEQIA
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atarrhini, Hominidae, Homo.
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and mouse CRD-BP, in benign and
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Nielsen, J., Christiansen, J., Lykke-Andersen, J., Johnsen, A.H., Wewer, U.M. and Nielsen, F.C.
A family of insulin-like growth factor II mRNA-binding proteins represses translation in late development
Mol. Cell. Biol. 19 (2), 1262-1270 (1999)
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DEFINITION Sequence 7 from patent US 6576756. ACCESSION AR343075.1 G1:33738477 KEYWORDS TRAYSONCE. Unclassified. Unclassified. Unclassified. Unclassified. TITLE TOTATE TO 1946 JOURNAL AND SECONDER AND SET 17-AUG-2003 NEFFRENCE OR AR343075.1 G1:33738477 REFERENCE OR AR343075.1 G1:33738477 REFERENCE OR AR343075.1 G1:33738477 REFERENCE OR AR343075.1 G1:33738477 REFERENCE OR AR343075.1 G1:33738477 REFERENCE OR AR343075.1 G1:33738477 REFERENCE TO 1946 JOURNAL TOTATION OF	ORIGIN ORIGIN ORIGIN OUCLY Match 99.7%; Score 1941; DB 6; Length 1946; Best Local Similarity 100.0%; Pred. No. 0; Matches 1946; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 1946; Conservative 0; Mismatches 0; Indels 0; Gaps 0; OY	61 CCACCCAGAGGCGGGGGGGGGGGGGGGGGGGGGGGGGG	### ### ##############################	661 TTATGCATAAAGAGGCTAAGGACACCAAAACGGCTGACGAGGTTCCCCTGAAGATCCTGG 720 721 CCCATAATAACTTTGTAGGGCGTCTCATTGGCAAGGAAGG

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JOURNAL Patent: US 6297364-A 7 02-OCT-2001; FEATURES Location/Qualifiers Source 1. 1946 /organism="unknown" ORIGIN	Query Match Best Local Similarity 100.0%; Pred. No. 0; Matches 1946; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	77866666776677677667776666667866666787878787878787878787878787878787878666667866666	Qy 61 CCACCCAGAGGCCGGGGGGGGGGGGGGGGGGGGGGGGG		0 0	30			8 4 8 8	CACAA 54	541 AACAGACCCAGTCCAAGATAGACGTGCATAGGAAGAAGACGCAGGTGCAGCTGAAAAAG	Qy 601 CCATCAGTGTGCACTCCTCGAGGGCTGCTCCTCGGCTTGTAAGATGATCTTGGAGA 660 Db 601 CCATCAGTGTGCACTCCACCCTGAGGGCTGCTCCTCGGCTTGTAAGATGATCTTGGAGA 660		GGTAG	AGGAAGATACCGAGACAAAAATCACCATCTCCTCGTTGCAAGACCTTACCAACC	GGAAA GGAAA	Qy 901 TAATGAAAGTTCGGGAGGCCTATGAGAATGATGTGGCTGCCATGAGCTCTCACCTGA 960

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SUMMARIES

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